





RESULT 4	ABG05086	RESULT 5	ABG05086
AB24498	AAB24498 standard; Protein; 58 AA.	ID	ABG05086 standard; Protein; 125 AA.
AC	AC	ID	ABG05086
XX	XX	ID	ABG05086
XX	XX	AC	ABG05086;
XX	XX	XX	XX
XX	XX	DE	Novel human diagnostic protein #5077.
DE	DE	XX	Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
XX	XX	XX	KW
Human; secreted protein; cytostatic; antianemic; antidiabetic; antiinflammatory; ophthalmological; antirheumatic; antiarthritic; KW			
antipsoriatic; antiangiogenic; cardiant; anti-HIV; nootropic; KW			
neuroprotective; antimicrobial; antiparkinsonian; cancer; KW			
immune system disorder; apoptosis; hyperproliferative disorder; KW			
cardiovascular disorder; apoptosis; neurological disease; KW			
infectious disease; wound healing.	OS	XX	OS
OS	OS	XX	Homo sapiens.
XX	XX	PN	WO200175067-A2.
XX	XX	PD	11-OCT-2001.
XX	XX	PR	30-MAR-2001; 2001WO-US08631.
XX	XX	PR	31-MAR-2001; 2000US-050217.
XX	XX	PR	23-AUG-2000; 2000US-0649167.
XX	XX	PR	17-DEC-1998; 98US-0112809.
XX	XX	PR	18-DEC-1998; 98US-0113006.
XX	XX	PA	(HYSE-) HYSEQ INC.
XX	XX	PA	Dramanac RT, Liu C, Tang YT;
XX	XX	PI	DR
XX	XX	DR	WPI; 2001-639362/73.
XX	XX	DR	N-PSDB; ASN6973.
XX	XX	PS	New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
XX	XX	PS	Claim 20; SEQ ID No 3445; 103pp; English.
XX	CC	CC	The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The
XX	CC	CC	polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed gene. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving
XX	CC	CC	polynucleotides are also used in diagnostics as expressed sequence tags (III). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity.
XX	CC	CC	The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG0010-ABG3037 represent novel human diagnostic amino acid sequences of the invention.
XX	CC	CC	Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at <a href="http://wipo.int/pub/published_pcr_sequences">http://wipo.int/pub/published_pcr_sequences</a> .
XX	XX	XX	Sequence 125 AA;
SQ	SQ	Query Match	17.2%; Score 27; DB 22; Length 125;
		Best Local Similarity	30.8%; Pred. No. 2.3e+03;
		Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;	QY 17 PXXXXXXCGXCGX 29
QY	QY	Best Local Similarity	30.8%; Pred. No. 1.3e+03; Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Db	Db	Db	13 PKGALLSACSGAC 25

ID AAU19418 standard; Protein; 274 AA.  
 XX  
 AC AAU19418;  
 XX  
 DT 04-DEC-2001 (first entry)  
 XX  
 DE Human diagnostic and therapeutic polypeptide (DITHP) #4.  
 XX  
 KW Human; receptor; diagnostic; therapeutic; gene therapy; vaccine;  
 KW cell proliferative disorder; Crohn's disease; lymphoma; leukaemia;  
 KW acquired immune deficiency syndrome; AIDS; autoimmune disorder;  
 KW respiratory disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200162927-A2.  
 XX  
 PD 30-AUG-2001.  
 XX  
 PR 21-FEB-2001; 2001WO-US06059.  
 PR  
 XX  
 PR 24-FEB-2000; 2000US-0184693.  
 PR  
 PR 24-FEB-2000; 2000US-0184697.  
 PR  
 PR 24-FEB-2000; 2000US-0184698.  
 PR  
 PR 24-FEB-2000; 2000US-0184768.  
 PR  
 PR 24-FEB-2000; 2000US-0184769.  
 PR  
 PR 24-FEB-2000; 2000US-0184770.  
 PR  
 PR 24-FEB-2000; 2000US-0184771.  
 PR  
 PR 24-FEB-2000; 2000US-0184776.  
 PR  
 PR 24-FEB-2000; 2000US-0184777.  
 PR  
 PR 24-FEB-2000; 2000US-0184797.  
 PR  
 PR 24-FEB-2000; 2000US-0184813.  
 PR  
 PR 24-FEB-2000; 2000US-0184837.  
 PR  
 PR 24-FEB-2000; 2000US-0185213.  
 PR  
 PR 24-FEB-2000; 2000US-0185216.  
 PR  
 PR 12-MAY-2000; 2000US-0203185.  
 PR  
 PR 15-MAY-2000; 2000US-0204226.  
 PR  
 PR 16-MAY-2000; 2000US-0204525.  
 PR  
 PR 16-MAY-2000; 2000US-0204621.  
 PR  
 PR 16-MAY-2000; 2000US-0205908.  
 PR  
 PR 17-MAY-2000; 2000US-0205932.  
 PR  
 PR 17-MAY-2000; 2000US-0204815.  
 PR  
 PR 17-MAY-2000; 2000US-0204863.  
 PR  
 PR 17-MAY-2000; 2000US-0205321.  
 PR  
 PR 17-MAY-2000; 2000US-0205385.  
 PR  
 PR 17-MAY-2000; 2000US-0205286.  
 PR  
 PR 17-MAY-2000; 2000US-0205287.  
 PR  
 PR 17-MAY-2000; 2000US-0205231.  
 PR  
 PR 17-MAY-2000; 2000US-0205324.  
 XX  
 PA (INCY) INCYTE GENOMICS INC.  
 XX  
 PI Panzer SR, Spiro PA, Bawville SC, Shah P, Chalup MS, Chang SC;  
 PI Chen A, D'Sa SK, Amshey S, Dahl CR, Dam TC, Daniels SE;  
 PI Durfour GE, Flores V, Fong WT, Greenawalt LB, Hillman JL, Jones AL;  
 PI Liu TF, Roseberry AM, Rosen BH, Russo FD, Stockdrehler TK, Daffo A;  
 PI Wright RJ, Yap PE, Yu JV, Bradley DL, Bratcher SR, Chen W;  
 PI Cohen HJ, Hodges DM, Lincoln SE, Jackson S;  
 DR WPI; 2001-502867/55.  
 DR N-PSDB; AAS30989.  
 XX  
 PT Polynucleotides encoding diagnostic and therapeutic proteins, e.g.  
 PT enzymes, hormones and receptors, useful in diagnostics and therapeutics  
 XX  
 PS Claim 27; Page 399-400; 522PP; English.  
 XX  
 CC The invention relates to polynucleotides (I) encoding diagnostic and

CC therapeutic (DITHP) polypeptides (II), which include e.g. enzymes, CC and proteins involved in growth and development and receptors. (I) and CC (II) may be used in the prevention, diagnosis and treatment of diseases CC associated with inappropriate DITHP expression. For example, (I) and CC (II) may be used to treat disorders associated with decreased polypeptide CC expression by rectifying mutations or deletions in a patient's genome, CC that affect the activity of the DITHPs, by expressing inactive proteins CC or supplementing the patient's own production of them. (I) and (II) CC may be used to treat diseases, for example, cell proliferative disorder, CC Crohn's disease, acquired immune deficiency syndrome (AIDS), lymphoma, CC leukaemia, autoimmune disorders, and respiratory disorders. Additionally, CC (I) may be used to produce the DITHPs, by inserting the nucleic acids CC into a host cell and culturing the cell to express the protein. (I) and CC its complementary sequences may also be used as DNA probes in diagnostic CC assays to detect and quantitate the presence of similar nucleic acids in CC samples and therefore which patients may be in need of restorative CC therapy. (II) may also be used as antigens in the production of antibodies against DITHPs and in assays to identify modulators of DITHP CC expression and activity. The anti-DITHP antibodies and antagonists may CC also be used to down regulate expression and activity. The anti-DITHP CC antibodies may also be used as diagnostic agents for detecting the CC presence of DITHPs in samples (e.g. by enzyme linked immunosorbant CC assay (ELISA)). AAU19418-AAU19625 represent human diagnostic and therapeutic (DITHP) polypeptides of the invention.

XX  
 SQ Sequence 274 AA;  
 XX  
 Query Match 30.8%; Score 27; DB 22; Length 274;  
 Best Local Similarity 30.8%; Pred. No. 3 4e+03;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
 QY 17 PXXXXXXGXC 29  
 Db 262 PCGSSSATCGHC 274

RESULT 7  
 ID AAB24499  
 XX  
 AC AAB24499;  
 XX  
 DT 20-NOV-2000 (first entry)  
 XX  
 DE Human secreted protein sequence encoded by gene 7 SEQ ID NO:125.  
 XX  
 KW Human; secreted Protein; cytostatic; antianaemic; antidiabetic;  
 KW antiinflammatory; ophthalmological; antiheumatic; antiarthritic;  
 KW antipsoriatic; antidiarrhoeal; cardiotonic; anti-HIV; nootropic;  
 KW neuroprotective; antimicrobial; antiparkinsonian; cancer;  
 KW immun system disorder; angiogenesis; hyperproliferative disorder;  
 KW cardiovascular disorder; apoptosis; neurological disease;  
 KW infectious disease; wound healing.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200005937-A1.

XX  
 PD 22-JUN-2000.  
 XX  
 PR 16-DEC-1999; 99WO-US29950.  
 PR  
 XX  
 PR 17-DEC-1998; 98US-0112809.  
 PR 18-DEC-1998; 98US-0113006.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Ruben SM, Ebner R, Rosen CA, Endress GA, Soppet DR, Ni J;  
 PI Duan DR, Moore PA, Shi Y, Lafleur DW, Olsen HS, Florence K;  
 XX  
 DR WPI; 2000-431566/37.

XX  
 Forty seven human nucleic acids encoding secreted proteins, useful in

PT the treatment, prevention and diagnosis of cancers, disorders of the  
 PT immune system, angiogenesis disorders, neurological diseases and  
 PT hyperproliferative disorders -  
 XX Disclosure: Page 25-26; 562pp; English.

CC The polynucleotide sequence given in AAT78381 to AAT70432 encode the  
 CC human secreted proteins given in AAB24437 to AAB4604. Human secreted  
 CC proteins have activities based on the tissues and cells the genes are  
 CC expressed in. Examples of activities include: cytostatic; antianemic;  
 CC antiangiogenic; antidiabetic; antidiarrhetic; antidiabetic; antihypertensive;  
 CC antiinflammatory; antidiabetic; antidiarrhetic; antidiabetic; anti-HIV;  
 CC nootropic; neuroprotective; antimicrobial and anti-parkinsonian.  
 CC Human secreted protein polynucleotides, polypeptides, antagonists and/or  
 CC agonists may be useful in treating, preventing, and/or diagnosing other  
 CC diseases, disorder, and/or conditions such as: (a) cancers; (b)  
 CC disorders of the immune system; (c) angiogenesis disorders; (d)  
 CC hyperproliferative disorders; (e) diseases  
 CC associated with increase apoptosis; (g) neurological diseases; and  
 CC (h) infectious diseases. They are also used to promote wound healing.  
 CC exemplification of the present invention.

XX Sequence 468 AA;

Query Match 17.2%; Score 27; DB 21; Length 468;  
 Best Local Similarity 30.8%; Pred. No. 4.8e+03; Mismatches 9; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Qv 17 PXXXXXXCGXC 29

Db 8 PGAAAGACLGAC 20

RESULT 8  
 ABB39643  
 ID ABB39643 standard; Peptide: 59 AA.

AC ABB39643;  
 XX  
 XX  
 DT 04-FEB-2002 (first entry)

DE Peptide #7149 encoded by human foetal liver single exon probe.  
 KW Human; foetal liver; gene expression; single exon nucleic acid probe.

OS Homo sapiens.  
 XX  
 WO200157277-A2.

XX  
 PD 09-AUG-2001.

PP 30-JAN-2001; 2001WO-US00666.

XX  
 PR 04-FEB-2000; 2000US-0180312.  
 PR 26-MAR-2000; 2000US-0207456.  
 PR 30-JUN-2000; 2000US-060408.  
 PR 03-AUG-2000; 2000US-0622366.  
 PR 21-SEP-2000; 2000US-0234687.  
 PR 27-SEP-2000; 2000US-0286359.  
 PR 04-OCT-2000; 2000GB-0024263.

XX  
 PA (MOL-) MOLECULAR DYNAMICS INC.  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX  
 DR WPI; 2001-488899/53.

XX  
 PT Single exon nucleic acid probes for analyzing gene expression in human  
 PT hearts -  
 XX  
 PS Claim 15; SEQ ID No 26094; 530pp; English.

XX  
 CC The present invention relates to single exon nucleic acid probes for  
 CC measuring human gene expression in a sample derived from human heart (see  
 CC ABA21535-ABA41305). The present sequence is a protein encoded by one such  
 CC probe. The probes may be used for predicting, measuring and displaying  
 CC gene expression in samples derived from the human heart via microarrays.  
 CC By measuring gene expression, the probes are useful for predicting,  
 CC diagnosing, grading, monitoring and prognosis diseases of the  
 CC human heart and vascular system e.g. cardiovascular disease,  
 CC hypertension, cardiac arrhythmias and congenital heart disease.  
 CC Note: the sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO

XX  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX  
 DR WPI; 2001-483447/52.  
 XX  
 PT Human genome-derived single exon nucleic acid probes useful for  
 PT analyzing gene expression in human fetal liver -  
 XX  
 PS Claim 27; SEQ ID NO 32278; 639pp + sequence listing; English.

CC The invention relates to a single exon nucleic acid probe for  
 CC measuring human gene expression in a sample derived from human foetal  
 CC liver. The single exon nucleic acid probes may be used for predicting,  
 CC measuring and displaying gene expression in samples derived from human  
 CC fetal liver. The present sequence is a peptide encoded by a single exon  
 CC nucleic acid probe of the invention.  
 CC Note: The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://ftp.wipo.int/pub/published_pct_sequences).

CC Sequence 59 AA;  
 ID ABB24324  
 XX  
 AC ABB24324;  
 XX  
 DT 23-JAN-2002 (first entry)

XX  
 PR Protein #6323 encoded by probe for measuring heart cell gene expression.  
 KW Human; gene expression; heart; microarray; vascular system;  
 KW cardiovascular disease; hypertension; cardiac arrhythmia;  
 KW congenital heart disease.  
 OS Homo sapiens.  
 XX  
 PN WO200157274-A2.

XX  
 PD 09-AUG-2001.

PP 30-JAN-2001; 2001WO-US00666.

XX  
 PR 04-FEB-2000; 2000US-0180312.  
 PR 26-MAR-2000; 2000US-0207456.  
 PR 30-JUN-2000; 2000US-060408.

PR 03-AUG-2000; 2000US-0622366.  
 PR 21-SEP-2000; 2000US-0234687.  
 PR 27-SEP-2000; 2000US-0286359.  
 PR 04-OCT-2000; 2000GB-0024263.

XX  
 PA (MOL-) MOLECULAR DYNAMICS INC.  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX  
 DR WPI; 2001-488899/53.

XX  
 PT Single exon nucleic acid probes for analyzing gene expression in human  
 PT hearts -  
 XX  
 PS Claim 15; SEQ ID No 26094; 530pp; English.

CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX Sequence 59 AA;  
 SQ

Query Match	16.6%	Score	26;	DB	22;	Length	59;
Best Local Similarity	30.8%	Pred. No.	1.8e+03;				
Matches	4;	Conservative	0;	Mismatches	9;	Indels	0;
						Gaps	0;

Qy 17 PXXXXXXCAGXC 29  
 Db 20 PGSSPPSACAGAC 32

RESULT 10  
 AAM60355  
 ID AAM60355 standard; Protein; 59 AA.  
 XX  
 AC AAM60355;  
 XX  
 DT 05-NOV-2001 (first entry)  
 DE Human brain expressed single exon probe encoded protein SEQ ID NO: 32460.  
 XX  
 KW Human; brain expressed exon; gene expression analysis; probe;  
 microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;  
 epilepsy; cancer.  
 XX  
 OS Homo sapiens.  
 PN WO200157275-A2.  
 XX  
 PD 09-AUG-2001.  
 XX  
 PF 30-JAN-2001; 2001WO-US00668.  
 XX  
 PR 04-FEB-2000; 2000US-0180312.  
 PR 26-MAY-2000; 2000US-0207456.  
 PR 30-JUN-2000; 2000US-0608408.  
 PR 03-AUG-2000; 2000US-0632366.  
 PR 21-SEP-2000; 2000US-0234887.  
 PR 27-SEP-2000; 2000US-0236359.  
 PR 04-OCT-2000; 2000GB-0024263.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 PT Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX  
 DR WPI; 2001-488900/53.  
 XX  
 PR Human genome-derived single exon nucleic acid probes useful for  
 analyzing gene expression in human bone marrow -  
 XX  
 PS Example 4: SEQ ID NO: 33297; 658pp + Sequence Listing; English.  
 XX  
 CC The present invention provides a number of single exon nucleic acid  
 probes which are derived from genomic sequences expressed in the human  
 bone marrow. They can be used to measure gene expression in bone marrow  
 samples, which may enable the improved diagnosis and treatment of cancers  
 such as lymphoma, leukaemia and myeloma. The present sequence is a  
 protein encoded by one of the probes of the invention.  
 XX  
 SQ Sequence 59 AA;  
 PT Single exon nucleic acid probes for analyzing gene expression in human  
 PT brains -  
 XX  
 PS Example 4; SEQ ID NO: 32460; 650pp + Sequence Listing; English.  
 XX  
 CC The present invention provides a number of single exon nucleic acid  
 probes which are derived from genomic sequences expressed in the human  
 brain. They can be used to measure gene expression in brain cell samples,  
 which may enable the diagnosis and improved treatment of nervous system  
 diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,  
 epilepsy and cancers. The present sequence is a protein encoded by one of  
 the probes of the invention.  
 XX  
 SQ Sequence 59 AA;  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX Sequence 59 AA;  
 SQ

Query Match	16.6%	Score	26;	DB	22;	Length	59;
Best Local Similarity	30.8%	Pred. No.	1.8e+03;				
Matches	4;	Conservative	0;	Mismatches	9;	Indels	0;
						Gaps	0;

Qy 17 PXXXXXXCAGXC 29  
 Db 20 PGSSPPSACAGAC 32

RESULT 11  
 AAM72991  
 ID AAM72991 standard; Protein; 59 AA.  
 XX  
 AC AAM72991;  
 XX  
 DT 06-NOV-2001 (first entry)  
 DE Human bone marrow expressed probe encoded protein SEQ ID NO: 33297.  
 XX  
 KW Human; bone marrow expressed exon; gene expression analysis; probe;  
 microarray; cancer; leukaemia; lymphoma; myeloma.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO20157276-A2.  
 XX  
 PR 03-AUG-2001.  
 XX  
 PR 30-JAN-2001; 2001WO-US00668.  
 XX  
 PR 04-FEB-2000; 2000US-0180312.  
 PR 26-MAY-2000; 2000US-0207456.  
 PR 30-JUN-2000; 2000US-0608408.  
 PR 03-AUG-2000; 2000US-0632366.  
 PR 21-SEP-2000; 2000US-0234887.  
 PR 27-SEP-2000; 2000US-0236359.  
 PR 04-OCT-2000; 2000GB-0024263.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 PT Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX  
 DR WPI; 2001-488900/53.  
 XX  
 PR Human genome-derived single exon nucleic acid probes useful for  
 analyzing gene expression in human bone marrow -  
 XX  
 PS Example 4: SEQ ID NO: 33297; 658pp + Sequence Listing; English.  
 XX  
 CC The present invention provides a number of single exon nucleic acid  
 probes which are derived from genomic sequences expressed in the human  
 bone marrow. They can be used to measure gene expression in bone marrow  
 samples, which may enable the improved diagnosis and treatment of cancers  
 such as lymphoma, leukaemia and myeloma. The present sequence is a  
 protein encoded by one of the probes of the invention.  
 XX  
 SQ Sequence 59 AA;  
 PT Single exon nucleic acid probes for analyzing gene expression in human  
 PT brains -  
 XX  
 PS Example 4; SEQ ID NO: 32460; 650pp + Sequence Listing; English.  
 XX  
 CC The present invention provides a number of single exon nucleic acid  
 probes which are derived from genomic sequences expressed in the human  
 brain. They can be used to measure gene expression in brain cell samples,  
 which may enable the diagnosis and improved treatment of nervous system  
 diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,  
 epilepsy and cancers. The present sequence is a protein encoded by one of  
 the probes of the invention.  
 XX  
 SQ Sequence 59 AA;  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX Sequence 59 AA;  
 SQ

Query Match	16.6%	Score	26;	DB	22;	Length	59;
Best Local Similarity	30.8%	Pred. No.	1.8e+03;				
Matches	4;	Conservative	0;	Mismatches	9;	Indels	0;
						Gaps	0;

Qy 17 PXXXXXXCAGXC 29  
 Db 20 PGSSPPSACAGAC 32

RESULT 12  
 AAM19796  
 ID AAM19796 standard; Protein; 59 AA.  
 XX  
 AC AAM19796;  
 XX  
 DT 12-OCT-2001 (first entry)  
 DE Peptide #6230 encoded by probe for measuring cervical gene expression.  
 KW Probe; human; microarray; gene expression; cervical epithelial cell;  
 KW cervical cancer.  
 XX  
 OS Homo sapiens.

PN WO20015278-A2.  
 XX  
 PR 09-AUG-2001.  
 PD  
 XX  
 PR 30-JAN-2001; 2001WO-US00670.  
 XX  
 PR 04-FEB-2000; 2000US-0180312.  
 XX  
 PR 26-MAY-2000; 2000US-0207456.  
 PR 30-JUN-2000; 2000US-0608408.  
 PR 03-AUG-2000; 2000US-0632366.  
 PR 21-SEP-2000; 2000US-0234687.  
 PR 27-SEP-2000; 2000US-0236359.  
 PR 04-OCT-2000; 2000GB-0024263.  
 XX  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX  
 DR WPI; 2001-488897/53.  
 XX  
 PR Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells -  
 PT Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells -  
 PS  
 XX  
 CC The present invention relates to human single exon nucleic acid probes (SENPs; see AAI1068-AA12845). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.  
 CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp://wipo.int/pub/published\\_pct\\_sequences](ftp://wipo.int/pub/published_pct_sequences).  
 XX  
 SQ Sequence 59 AA:  
 XX  
 CC Query Match 16.6%; Score 26; DB 22; Length 59;  
 CC Best Local Similarity 30.8%; Pred. No. 1.8e+03;  
 CC Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
 CC  
 CC Db 20 PGSSPPSACAGAC 32  
 XX  
 AC RESULT 14  
 XX  
 AC ABG42830 standard; Peptide; 59 AA.  
 XX  
 AC ABG42830;  
 XX  
 DT 19-AUG-2002 (first entry)  
 XX  
 DE Human peptide encoded by genome-derived single exon probe SEQ ID 32495.  
 XX  
 KW Human; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberosis sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangiomyomatosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocytic pulmonary dysplasia; primary ciliary dyskinesia; pulmonary hypertension; hyaline membrane disease.  
 KW  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200186003-A2.  
 XX  
 PD 15-NOV-2001.  
 XX  
 PR 30-JAN-2001; 2001WO-US00665.  
 XX  
 PR 04-FEB-2000; 2000US-180312P.  
 PR 26-MAY-2000; 2000US-207456P.  
 PR 30-JUN-2000; 2000US-0608408.  
 PR 03-AUG-2000; 2000US-0632366.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-234687P.  
 PR 04-OCT-2000; 2000GB-0024263.  
 XX  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;

DR WPI; 2002-114183/15.  
 XX KW acute spinal cord injury; multiple sclerosis; eosinopenia; lymphopenia;  
 XX KW monocytopenia; neutropenia; anaemia; thrombocytopenia; neuroblastoma;  
 PT Spatially addressable set of single exon nucleic acid probes, used to KW antibody; obesity; therapy; bone morphogenic factor 3; growth factor;  
 PT measure gene expression in human lung samples - KW hybrid protein; BMP3.  
 XX PS Claim 27; SEQ ID NO 32495; 634pp; English.  
 XX  
 CC The invention relates to a spatially-addressable set of single exon  
 CC nucleic acid probes for measuring gene expression in a sample derived  
 CC from human lung comprising single exon nucleic acid probes having one of  
 CC 12614 nucleic acid sequences mentioned in the specification, or their  
 CC complements or the 12387 open reading frames derived from the 12614  
 CC probes. Also included are a microarray comprising the novel set of  
 CC probes; the novel set of probes which hybridise at high stringency to a  
 CC nucleic acid expressed in the human lung; measuring gene expression in a  
 CC sample derived from human lung, comprising (a) contacting the array with  
 CC mRNA, and (b) measuring the label detectably bound to each probe of  
 CC the array; identifying exons in a eukaryotic genome, comprising  
 CC (a) algorithmically predicting at least one exon from genomic sequences  
 CC of the eukaryote; and (b) detecting specific hybridisation of detectably  
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,  
 CC having a fragment identical to the predicted exon, the probe is included  
 CC in the above mentioned microarray; assigning exons to a single gene  
 CC comprising (a) identifying exons from genomic sequence by the method  
 CC above and (b) measuring the expression of each of the exons in several  
 CC tissues and/or cell types using hybridisation to a single exon  
 CC microarray having a probe with the exon, where a common pattern of  
 CC expression of the exons in the tissues and/or cell types indicates that  
 CC the exons should be assigned to a single gene; a peptide comprising one  
 CC of 12011 sequences, mentioned in the specification, or encoded by the  
 CC probes/open reading frames (ORF). The probes are used for gene  
 CC expression analysis and for identifying exons in a gene particularly  
 CC using human lung derived mRNA and for the study of lung diseases  
 CC such as asthma, lung cancer, chronic obstructive pulmonary disease  
 CC (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary  
 CC fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease,  
 CC Niemann-pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary  
 CC haemangiopericytoma, pulmonary histiocytosis, lymphangioliomoyomatosis,  
 CC pulmonary alveolar proteinosis, Kartagener syndrome, fibrocytic  
 CC pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension  
 CC and hyaline membrane disease. The present sequence is a peptide/protein  
 CC encoded by a single exon probe of the invention.  
 Note: The sequence data for this patient did not form part  
 CC of the printed specification, but was obtained in electronic  
 CC format directly from WIPO at  
 CC ftp://wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 59 AA;  
 CC Query Match 16.6%; Score 26; DB 23; Length 59;  
 CC Best Local Similarity 30.8%; Pred. No. 1.8e+03;  
 CC Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
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 Db 20 PGSSPPSACAGAC 32  
 XX  
 RESULT 15  
 AAW30345  
 ID AAW30345 standard; Peptide; 66 AA.  
 XX  
 AAW30345;  
 XX  
 DT 11-FEB-1998 (first entry)  
 XX  
 DE Fragment of bone morphogenic factor 3.  
 XX  
 KW Neurturin; human; haematopoietic cell; neuronal cell; stem cell; NT gene;  
 KW neurodegenerative disease; peripheral neuropathy; nervous system tumour;  
 KW amyotrophic lateral sclerosis; Alzheimer's disease; Parkinson's disease;  
 KW Huntington's disease; ischaemic stroke; acute brain injury; basophaenia;

KW acute spinal cord injury; multiple sclerosis; eosinopenia; lymphopenia;  
 KW KW monocytopenia; neutropenia; anaemia; thrombocytopenia; neuroblastoma;  
 KW antibody; obesity; therapy; bone morphogenic factor 3; growth factor;  
 KW hybrid protein; BMP3.  
 XX OS Homo sapiens.  
 XX WO9708196-A1.  
 XX PN 05-MAR-1997.  
 XX PR 27-AUG-1996; 96WO-US14055.  
 XX PR 28-AUG-1995; 95US-0519777.  
 XX PA (UNIW ) UNIV WASHINGTON.  
 XX PI Johnson EM, Kotzbauer PT, Lampe PA, Milbrandt JD;  
 XX DR WPI; 1997-179176/16.  
 XX A novel growth factor Neurturin - used to treat neuro-degenerative  
 PT and haematopoietic cell degeneration diseases, e.g. Alzheimer's  
 PT disease and eosinopenia.  
 XX PS Claim 93; Fig 17; 206pp; English.  
 XX  
 CC AAW30331-W30353 represent human growth factor fragments that are used in  
 CC a hybrid polypeptide of the invention. These sequences form a hybrid  
 CC with the human neurturin (NT) fragment shown in AAW3078. NT promotes the  
 CC growth and differentiation of haematopoietic and neuronal cells, and  
 CC their stem cells. The NT gene and protein are used to prevent or treat  
 CC neurodegenerative diseases e.g. peripheral neuropathy, amyotrophic  
 CC lateral sclerosis, Alzheimer's disease, Parkinson's disease,  
 CC Huntingdon's disease, ischaemic stroke, acute brain injury, acute spinal  
 CC cord injury, nervous system tumours, multiple sclerosis and infection;  
 CC and haematopoietic cell degenerative diseases, e.g. eosinopenia,  
 CC basophaenia, lymphopenia, monocytopenia, neutropenia, anaemia,  
 CC thrombocytopenia and stem cell insufficiencies. The NT protein and gene  
 CC are also useful to treat neuroblastomas. Antibodies against NT and  
 CC oligonucleotides (used as either probes or primers, corresponding to an  
 CC exon of pre-pro-NT gene or flanking a target sequence) can be used for  
 CC detecting NT in a sample or detecting mutations in the NT gene. Antisense  
 CC sequences of the NT gene are used to treat diseases promoted by NT  
 CC expression e.g. obesity.  
 XX SQ Sequence 66 AA;  
 CC Query Match 16.6%; Score 26; DB 18; Length 66;  
 CC Best Local Similarity 30.8%; Pred. No. 2e+03;  
 CC Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
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 Db 22 PRSFDAYCSCAC 34  
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 Job time : 38 secs

GenCore version 5.1.4-p5, 4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

March 27, 2003, 10:59:00 ; Search time 15 Seconds

(without alignments)

190.268 Million cell updates/sec

Title: US-09-828-607-6  
Perfect score: 157

Sequence: 1 XXXXXXXXXXXXXXXXXX 97

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Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 23422922 residues

Total number of hits satisfying chosen parameters: 262574

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Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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4	26	16.6	103	4	US-08-931-164
5	26	16.6	103	4	US-08-981-739-164
6	26	16.6	103	4	US-09-128-020-164
7	26	16.6	104	1	US-08-278-26
8	26	16.6	104	1	US-08-155-343A-26
9	26	16.6	104	1	US-08-406-671-26
10	26	16.6	104	1	US-08-643-763A-26
11	26	16.6	104	1	US-08-643-763A-26
12	26	16.6	104	1	US-08-462-623-26
13	26	16.6	104	2	US-08-451-952A-26
14	26	16.6	104	2	US-08-445-468A-26
15	26	16.6	104	2	US-08-461-391A-26
16	26	16.6	104	2	US-08-918-26
17	26	16.6	104	3	US-08-278-730A-26
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20	26	16.6	104	4	US-08-271-550A-13
21	26	16.6	104	4	US-09-170-936-26
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23	26	16.6	104	5	PCT-US93-07190-26
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#### ALIGNMENTS

RESULT 1	US-09-072-596-297	Sequence 21, Appl
	Sequence 297, Appl	Sequence 17, Appl
	Patent No. 6458366	Sequence 25, Appl
	GENERAL INFORMATION:	Sequence 21, Appl
	APPLICANT: Read, Steven G.	Sequence 18, Appl
	APPLICANT: Skalky, Yasir A.W.	Sequence 16, Appl
	APPLICANT: Dillon, Davin C.	Sequence 16, Appl
	APPLICANT: Campos Neto, Antonia	Sequence 16, Appl
	APPLICANT: Houghton, Raymond	Sequence 18, Appl
	APPLICANT: Vedvick, Thomas S.	Sequence 18, Appl
	APPLICANT: Twardzik, Daniel R.	Sequence 16, Appl
	APPLICANT: Loores, Michael J.	Sequence 16, Appl
	APPLICANT: Hendrickson, Ronald C.	Sequence 16, Appl
	TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF TUBERCULOSIS	Sequence 16, Appl
	NUMBER OF SEQUENCES: 350	Sequence 16, Appl
	CORRESPONDENCE ADDRESS:	Sequence 16, Appl
	ADRESSEE: SEED and BERRY LLP	Sequence 16, Appl
	CITY: Seattle	Sequence 16, Appl
	STATE: Washington	Sequence 16, Appl
	ZIP: 98104-092	Sequence 16, Appl
	ZIP: 98104-092	Sequence 16, Appl
	COMPILER READABLE FORM:	Sequence 16, Appl
	MEDIUM TYPE: FLOPPY DISK	Sequence 16, Appl
	COMPUTER: IBM PC COMPATIBLE	Sequence 16, Appl
	OPERATING SYSTEM: PC-DOS/MS-DOS	Sequence 16, Appl
	SOFTWARE: Patentent Release #1.0, Version #1.30	Sequence 16, Appl
	CURRENT APPLICATION DATA:	Sequence 16, Appl
	APPLICATION NUMBER: US/09/072,596	Sequence 16, Appl
	FILING DATE: 05-MAY-1998	Sequence 16, Appl
	CLASSIFICATION:	Sequence 16, Appl
	ATTORNEY/AGENT INFORMATION:	Sequence 16, Appl
	NAME: Maki, David J.	Sequence 16, Appl
	REGISTRATION NUMBER: 31,392	Sequence 16, Appl
	REFERENCE/DOCKET NUMBER: 210121.417C9	Sequence 16, Appl
	TELECOMMUNICATION INFORMATION:	Sequence 16, Appl
	TELEPHONE: (206) 622-4900	Sequence 16, Appl
	TELEFAX: (206) 682-6031	Sequence 16, Appl
	INFORMATION FOR SEQ ID NO: 297:	Sequence 16, Appl
	SEQUENCE CHARACTERISTICS:	Sequence 16, Appl
	LENGTH: 178 amino acids	Sequence 16, Appl
	TYPE: amino acid	Sequence 16, Appl
	STRANDEDNESS: single	Sequence 16, Appl
	TOPOLOGY: linear	Sequence 16, Appl
	MOLECULE TYPE: protein	Sequence 16, Appl
	US-09-072-596-297	Sequence 16, Appl

Query Match	17.8%	Score 28; DB 4; Length 178;
Best Local Similarity	30.8%	Pred. No. 3.4e+02;



OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/931,858E  
 FILING DATE:  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: HOLLAND, DONALD R.  
 REGISTRATION NUMBER: 35,197  
 REFERENCE/DOCKET NUMBER: 971486  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 314-727-5188  
 FAX: 314-727-6092  
 INFORMATION FOR SEQ ID NO: 164:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 103 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLogy: linear  
 MOLECULE TYPE: peptide  
 US-08-931-858E-164

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 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
 Sequence 164, Application US/08981739  
 Patent No. 6232449

GENERAL INFORMATION:  
 APPLICANT: MILLERANDT, JEFFREY D.  
 LAMMEL, PATRICIA A.  
 KOTZBAUER, PAUL T.  
 KOTZBAUER, PAUL T.  
 LAMMEL, PATRICIA A.  
 MILLERANDT, JEFFREY D.

APPLICANT: MILLERANDT, JEFFREY D.  
 APPLICANT: KOTZBAUER, PAUL T.  
 APPLICANT: LAMMEL, PATRICIA A.  
 TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS  
 NUMBER OF SEQUENCES: 176  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: HOWELL & HAERKAMP, L.C.  
 STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
 CITY: ST. LOUIS  
 STATE: MISSOURI  
 COUNTRY: US  
 ZIP: 63105-1817

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/128,026  
 FILING DATE:

ATTORNEY/AGENT INFORMATION:  
 NAME: HOLLAND, DONALD R.  
 REGISTRATION NUMBER: 35,197  
 REFERENCE/DOCKET NUMBER: 9716163  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (314) 727-5188  
 TELEFAX: (314) 727-6092  
 INFORMATION FOR SEQ ID NO: 164:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 103 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLogy: linear  
 MOLECULE TYPE: peptide  
 US-09-128-026-164

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 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
 Sequence 26, Application US/08278729A  
 Patent No. 5650276

GENERAL INFORMATION:  
 APPLICANT: SMART, JOHN  
 APPLICANT: OPPERMANN, HERMAN

INFORMATION FOR SEQ ID NO: 164:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 103 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single

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 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
 Sequence 164, Application US/09128026  
 Patent No. 6403335

GENERAL INFORMATION:  
 APPLICANT: JOHNSON JR., EUGENE M.  
 MILLERANDT, JEFFREY D.  
 APPLICANT: MILLERANDT, JEFFREY D.  
 APPLICANT: LAMMEL, PATRICIA A.  
 TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS  
 NUMBER OF SEQUENCES: 176  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: HOWELL & HAERKAMP, L.C.  
 STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
 CITY: ST. LOUIS  
 STATE: MISSOURI  
 COUNTRY: US  
 ZIP: 63105-1817

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/128,026  
 FILING DATE:

ATTORNEY/AGENT INFORMATION:  
 NAME: HOLLAND, DONALD R.  
 REGISTRATION NUMBER: 35,197  
 REFERENCE/DOCKET NUMBER: 9716163  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (314) 727-5188  
 TELEFAX: (314) 727-6092  
 INFORMATION FOR SEQ ID NO: 164:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 103 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLogy: linear  
 MOLECULE TYPE: peptide  
 US-09-128-026-164

RESULT 7  
 US-08-278-729A-26





RESULT 12  
 US-08-462-623-26  
 Sequence 26, Application US/08462623  
 Patent No. 5739107  
 GENERAL INFORMATION:  
 APPLICANT: COHEN, CHARLES M.  
 APPLICANT: CHARETTE, MARC F.  
 APPLICANT: KUBERASAMPATH, THANGAVEL  
 APPLICANT: RUGGER, DAVID C.  
 APPLICANT: OPPERMANN, HERMANN  
 APPLICANT: PANG, ROY H.L.  
 APPLICANT: OZKAYNAK, ENGIN  
 COMPUTER READABLE FORM:  
 TITLE OF INVENTION: MORPHOGEN TREATMENT OF GASTROINTESTINAL  
 NUMBER OF SEQUENCES: 33  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES  
 STREET: 45 SOUTH STREET  
 CITY: HOPKINTON  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 01748  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY DISK  
 COMPUTER: IBM PC COMPATIBLE  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PATENTIN Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/462,623  
 FILING DATE: 26-MAY-1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: FENWICK, ESQ., GILIAN M.  
 REGISTRATION NUMBER: 36,508  
 REFERENCE/DOCKET NUMBER: CRP-074CN  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (508) 435-9001  
 TELEFAX: (508) 435-6951  
 INFORMATION FOR SEQ ID NO: 26:  
 LENGTH: 104 amino acids  
 SEQUENCE CHARACTERISTICS:  
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 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
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 Sequence 26, Application US/08445468A  
 Patent No. 5849686  
 GENERAL INFORMATION:  
 APPLICANT: KUBERASAMPATH, THANGAVEL  
 APPLICANT: RUGGER, DAVID C.  
 APPLICANT: OPPERMANN, HERMAN  
 APPLICANT: PANG, ROY H.L.  
 APPLICANT: COHEN, CHARLES M.  
 TITLE OF INVENTION: MORPHOGEN-INDUCED LIVER REGENERATION  
 NUMBER OF SEQUENCES: 33  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES  
 STREET: 45 SOUTH STREET  
 CITY: HOPKINTON  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 01748  
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 MEDIUM TYPE: FLOPPY DISK  
 COMPUTER: IBM PC COMPATIBLE  
 OPERATING SYSTEM: PC-DOS/MS-DOS

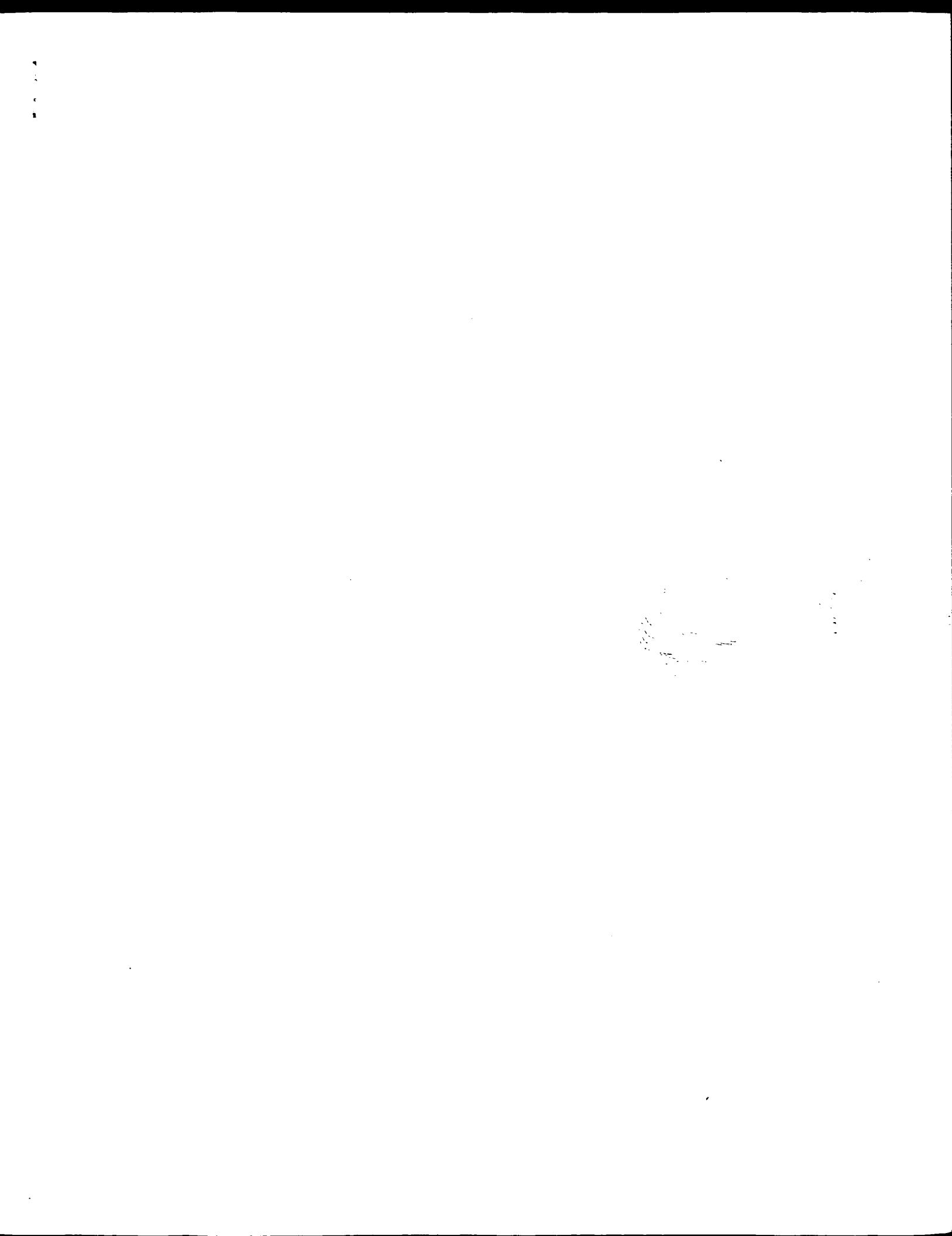
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 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: FENTON ESQ., GILLIAN M.  
 REGISTRATION NUMBER: 36,508  
 REFERENCE/DOCKET NUMBER: CRP-072FW2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 248-7100  
 FAX: (617) 248-7150  
 INFORMATION FOR SEQ ID NO: 26:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 104 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FEATURE:  
 NAME/KEY: Protein  
 LOCATION: 1..104  
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 US-08-445-468A-26

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 Job time : 16 secs

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 Sequence 26, Application US/08461397A  
 Patent No. 5,973,884  
 GENERAL INFORMATION:  
 APPLICANT: COHEN, CHARLES M.  
 APPLICANT: CHARETTE, MARC F.  
 APPLICANT: KUBERASAMPAATH, THANGAVEL  
 APPLICANT: RUEGER, DAVID C.  
 APPLICANT: OPPERMANN, HERMANN  
 APPLICANT: PANG, ROY H. L.  
 APPLICANT: OZKAYNAK, ENGIN  
 APPLICANT: SMART, JOHN E.  
 TITLE OF INVENTION: MORPHOGEN TREATMENT FOR LIMITING  
 NUMBER OF SEQUENCES: 33  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES  
 STREET: 45 SOUTH STREET  
 CITY: HOPKINTON  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 01748  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/461,397A  
 FILING DATE: 05-JUN-1995  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: PITCHER ESQ., EDMUND R.  
 REGISTRATION NUMBER: 27,829  
 REFERENCE/DOCKET NUMBER: CRP-074FW2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617/248-7000  
 FAX: 617/248-7100



Gencore version 5.1.4\_p5-4578  
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Run on:

March 27, 2003, 10:59:45 ; Search time 14 Seconds

(without alignments)  
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Perfect score: 157

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Total number of hits satisfying chosen parameters: 237916

Minimum DB seq length: 0

Maximum DB seq length: 200000000

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Maximum Match 100%

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Pred. No. 1 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
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2	27	17.2	2609	9 US-10-184-641-407 Sequence 407, App
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4	26	59	10 US-09-804-761-39622 Sequence 39622, A	
5	26	84	10 US-09-995-515-8 Sequence 8, App	
6	26	115	10 US-09-813-459-25 Sequence 25, App	
7	26	115	10 US-09-813-459-25 Sequence 26, App	
8	26	16.6	119 12 US-115-400-16 Sequence 16, App	
9	26	16.6	120 9 US-09-829-211-42 Sequence 42, App	
10	26	16.6	120 10 US-09-833-459-6 Sequence 20, App	
11	26	16.6	120 10 US-09-833-459-6 Sequence 6, App	
12	26	16.6	120 10 US-09-813-459-16 Sequence 16, App	
13	26	16.6	131 10 US-09-995-512 Sequence 12, App	
14	26	16.6	140 10 US-09-995-515-2 Sequence 2, App	
15	26	16.6	182 9 US-09-914-877-139 Sequence 139, App	
16	26	16.6	195 10 US-09-995-515-4 Sequence 4, App	
17	26	16.6	212 10 US-09-949-192-29 Sequence 29, App	
18	26	16.6	473 9 US-09-813-398-25 Sequence 25, App	
19	26	16.6	476 10 US-09-813-459-5 Sequence 5, App	

### ALIGNMENTS

#### RESULT 1

US-09-801-368-358

; Sequence 358, Application US/09801368

; Patent No. US2002128250A1

; GENERAL INFORMATION:

; APPLICANT: Busby, Robert

; APPLICANT: Call, Brian

; APPLICANT: Hecht, Peter

; APPLICANT: Holtzman, Doug

; APPLICANT: Madden, Kevin

; APPLICANT: Maxon, Mary

; APPLICANT: Milne, Todd

; APPLICANT: Royer, John

; APPLICANT: Salama, Sofie

; APPLICANT: Sherman, Amir

; APPLICANT: Silva, Jeff

; APPLICANT: Summers, Eric

; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi

; FILE REFERENCE: 109272-147

; CURRENT APPLICATION NUMBER: US/09/801-368

; CURRENT FILING DATE: 2001-03-07

; PRIORITY APPLICATION NUMBER: US 09/487-558

; PRIORITY FILING DATE: 2000-01-19

; PRIORITY APPLICATION NUMBER: US 60/160, 587

; NUMBER OF SEQ ID NOS: 440

; SOFTWARE: Patent version 3.0

; SEQ ID NO 358 LENGTH: 549

; TYPE: PRT

; ORGANISM: Aspergillus nidulans

US-09-801-368-358

Query Match 17.2%; Score 27; DB 10; Length 549;  
 Best Local Similarity 30.8%; Pred. No. 1.6e+03; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 9;

QY 17 PXXXXXXXXXXXX 29  
 Db 168 PAVIGSEGCTGSC 180

RESULT 2

US-10-184-644-407

; Sequence 407, Application US/10184644

; Publication No. US20030044930A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P34301C227

; CURRENT APPLICATION NUMBER: US/10/184,644

; CURRENT FILING DATE: 2002-05-28

; PRIOR APPLICATION removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 407

; LENGTH: 2609

; TYPE: DNA

; ORGANISM: Homo sapien

; US-10-184-644-407

Db 2823 CTGTCTTTAACTTTAACCTGAATATAATGATC 2860

; Sequence 39622, Application US/09864761

; Patent No. US20020048763A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharron G.

; APPLICANT: Rank, David R.

; APPLICANT: Hanzel, David K.

; APPLICANT: Chen, Wensheng

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO

; FILE REFERENCE: Ascom1ca-X1

; CURRENT APPLICATION NUMBER: US/09/864,761

; CURRENT FILING DATE: 2001-05-23

; PRIORITY APPLICATION NUMBER: US 60/180,312

; PRIORITY FILING DATE: 2000-02-04

; PRIORITY APPLICATION NUMBER: US 60/207,456

; PRIORITY FILING DATE: 2000-05-26

; PRIORITY APPLICATION NUMBER: US 09/632,366

; PRIORITY FILING DATE: 2000-08-03

; PRIORITY APPLICATION NUMBER: PCT/24263.6

; PRIORITY FILING DATE: 2000-10-04

; PRIORITY APPLICATION NUMBER: US 60/236,359

; PRIORITY FILING DATE: 2000-09-27

; PRIORITY APPLICATION NUMBER: PCT/US01/00666

; PRIORITY FILING DATE: 2001-01-30

; PRIORITY APPLICATION NUMBER: PCT/US01/00667

; PRIORITY FILING DATE: 2001-01-30

; PRIORITY APPLICATION NUMBER: PCT/US01/00668

; PRIORITY FILING DATE: 2001-01-30

; PRIORITY APPLICATION NUMBER: PCT/US01/00669

; PRIORITY FILING DATE: 2001-01-30

; PRIORITY APPLICATION NUMBER: PCT/US01/00665

; PRIORITY FILING DATE: 2001-01-30

; PRIORITY APPLICATION NUMBER: PCT/US01/00668

; PRIORITY FILING DATE: 2001-01-30

; PRIORITY APPLICATION NUMBER: PCT/US01/00663

; PRIORITY FILING DATE: 2001-01-30

; PRIORITY APPLICATION NUMBER: PCT/US01/00662

; PRIORITY FILING DATE: 2001-01-30

; PRIORITY APPLICATION NUMBER: PCT/US01/00661

; PRIORITY FILING DATE: 2001-01-30

; PRIORITY APPLICATION NUMBER: PCT/US01/00670

; PRIORITY FILING DATE: 2001-01-30

; PRIORITY APPLICATION NUMBER: US 60/234,687

; PRIORITY FILING DATE: 2000-09-21

; PRIORITY APPLICATION NUMBER: US 09/608,408

; PRIORITY FILING DATE: 2000-06-30

; PRIORITY APPLICATION NUMBER: US 09/774,203

; PRIORITY FILING DATE: 2001-01-29

; NUMBER OF SEQ ID NOS: 4917

; SOFTWARE: Annotrax Sequence Listing Engine vers. 1.1

; SEQ ID NO 39622

; LENGTH: 59

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: MAP TO AC005809.1

; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.1

; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.5

; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 66

; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.3

; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 8.4

; OTHER INFORMATION: EXPRESSED IN HELM, SIGNAL = 4.1

; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 6.4

; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 5.1

; OTHER INFORMATION: SWISSPROT HIT: 070942, EVALUE 1.60e-00

RESULT 3

US-10-184-644-407

; Sequence 407, Application US/10184644

; Publication No. US20030044930A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P34301C227

; CURRENT APPLICATION NUMBER: US/10/184,644

; CURRENT FILING DATE: 2002-05-28

; PRIOR APPLICATION removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 407

; LENGTH: 2870

; TYPE: DNA

; ORGANISM: Homo Sapien

; US-10-184-644-407

; Query Match 17.2%; Score 27; DB 9; Length 2870;

; Best Local Similarity 10.5%; Pred. No. 4.6e-03; Mismatches 4; Conservative 0; Indels 34; Gaps 0; Length 2870; Matches 25

; Cigar String: CGXGXXXXXXXXXXXXXXXXXXXX 62

Query Match<sup>n</sup> 16.6%; Score 26; DB 10; Length 59;  
 Best Local Similarity 30.8%; Pred. No. 5e+02; 25;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 17 PXXXXXXCXC 29  
 Db 20 PGSSPPSACAGAC 32

RESULT 5  
 US-09-995-515-8

GENERAL INFORMATION:  
 APPLICANT: Jing, Shiqian  
 TITLE OF INVENTION: Transforming Growth Factor-Beta-Related Molecules and  
 FILE REFERENCE: 00-659-A  
 CURRENT APPLICATION NUMBER: US/09/995, 515  
 CURRENT FILING DATE: 2001-11-28  
 PRIOR APPLICATION NUMBER: 60/253, 476  
 PRIOR FILING DATE: 2000-11-28  
 NUMBER OF SEQ ID NOS: 27  
 SOFTWARE: Patentin Ver. 2.0  
 SEQ ID NO 8  
 LENGTH: 84  
 TYPE: PRT  
 ORGANISM: Homo sapiens

Query Match<sup>n</sup> 16.6%; Score 26; DB 10; Length 84;  
 Best Local Similarity 30.8%; Pred. No. 6.4e+02; 25;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 17 PXXXXXXCXC 29  
 Db 56 PKMLSFSYCQGIC 68

RESULT 6  
 US-09-813-459-25  
 Sequence 25, Application US/09813459  
 GENERAL INFORMATION:  
 APPLICANT: Lee, Se-Jin  
 Cunningham, No. US20020107369A1  
 TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-10  
 NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Spensley Horn Jubas & Lubitz  
 STREET: 1880 Century Park East, Suite 500  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: USA  
 ZIP: 90067

COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/813,459  
 FILING DATE: 20-Mar-2001  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/624, 635  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Wetherell, Jr., Ph.D., John R.,  
 REGISTRATION NUMBER: 31,678  
 REFERENCE/DOCKET NUMBER: PD-3054

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619) 455-5100  
 TELEX: (619) 455-5110

INFORMATION FOR SEQ ID NO: 26:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 115 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 IMMEDIATE SOURCE:  
 CLONE: Human GDF-10  
 FEATURE:  
 NAME/KEY: Protein  
 LOCATION: 1..115

SEQUENCE DESCRIPTION: SEQ ID NO: 25:  
 US-09-813-459-25

Query Match<sup>n</sup> 16.6%; Score 26; DB 10; Length 115;  
 Best Local Similarity 30.8%; Pred. No. 7.9e+02; 25;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 17 PXXXXXXCXC 29  
 Db 34 PKSFDAYCAGAC 46

RESULT 7  
 US-09-813-459-26  
 Sequence 26, Application US/09813459  
 GENERAL INFORMATION:  
 APPLICANT: Lee, Se-jin  
 Cunningham, No. US20020107369A1  
 TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-10  
 NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Spensley Horn Jubas & Lubitz  
 STREET: 1880 Century Park East, Suite 500  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: USA  
 ZIP: 90067

COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/813,459  
 FILING DATE: 20-Mar-2001  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/624, 635  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Wetherell, Jr., Ph.D., John R.,  
 REGISTRATION NUMBER: 31,678  
 REFERENCE/DOCKET NUMBER: PD-3054

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619) 455-5100  
 TELEX: (619) 455-5110

INFORMATION FOR SEQ ID NO: 26:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 115 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 IMMEDIATE SOURCE:  
 CLONE: Murine GDF-10  
 FEATURE:  
 NAME/KEY: Protein  
 LOCATION: 1..115

SEQUENCE DESCRIPTION: SEQ ID NO: 26:

US-09-813-459-26

Query Match 16.6%; Score 26; DB 10; Length 115;  
 Best Local Similarity 30.8%; Pred. No. 7.9e+02; 9; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 9; SEQ ID NO 42  
 LENGTH: 120

Qy 17 PXXXXXXCGXC 29  
 Db 34 PKSFDAVYCGAC 46

RESULT 8  
 Sequence 16, Application US/10115406  
 Patent No. US2002122612A1

GENERAL INFORMATION:  
 APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE  
 APPLICANT: LEE, Se-Jin  
 TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-9  
 FILE REFERENCE: JHII190-3  
 CURRENT APPLICATION NUMBER: US/10/115,406

PRIOR APPLICATION NUMBER: 09/301,520  
 PRIOR FILING DATE: 1999-04-28  
 PRIOR APPLICATION NUMBER: US 09/172,062  
 PRIOR FILING DATE: 1998-10-13  
 PRIOR APPLICATION NUMBER: US 08/491,835  
 PRIOR FILING DATE: 1995-10-23  
 PRIOR APPLICATION NUMBER: PCT/US94/00685  
 PRIOR FILING DATE: 1994-01-12  
 PRIOR APPLICATION NUMBER: US 08/003,303  
 PRIOR FILING DATE: 1993-01-12  
 NUMBER OF SEQ ID NOS: 28  
 SOFTWARE: Patentin version 3.0  
 SEQ ID NO: 16  
 LENGTH: 119

TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-115-406-16

Query Match 16.6%; Score 26; DB 12; Length 119;  
 Best Local Similarity 30.8%; Pred. No. 8e+02; 9; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 9; SEQ ID NO 51  
 LENGTH: 120

Qy 17 PXXXXXXCGXC 29  
 Db 39 PKSFDAVYCGAC 51

PRIOR FILING DATE: 1993-03-19  
 NUMBER OF SEQ ID NOS: 51  
 SOFTWARE: FASTSEQ for Windows Version 4.0  
 SEQ ID NO 42  
 LENGTH: 120  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-859-211-42

Query Match 16.6%; Score 26; DB 9; Length 120;  
 Best Local Similarity 30.8%; Pred. No. 8.1e-02; 9; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 9; SEQ ID NO 51  
 LENGTH: 120  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-880-708-20

Query Match 16.6%; Score 26; DB 9; Length 120;  
 Best Local Similarity 30.8%; Pred. No. 8.1e-02; 9; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 9; SEQ ID NO 51  
 LENGTH: 120  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-880-708-20

Query Match 16.6%; Score 26; DB 9; Length 120;  
 Best Local Similarity 30.8%; Pred. No. 8.1e-02; 9; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 9; SEQ ID NO 51  
 LENGTH: 120  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-880-708-20

Query Match 16.6%; Score 26; DB 9; Length 120;  
 Best Local Similarity 30.8%; Pred. No. 8.1e-02; 9; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 9; SEQ ID NO 51  
 LENGTH: 120  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-880-708-20

Query Match 16.6%; Score 26; DB 9; Length 120;  
 Best Local Similarity 30.8%; Pred. No. 8.1e-02; 9; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 9; SEQ ID NO 51  
 LENGTH: 120  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-880-708-20

Query Match 16.6%; Score 26; DB 9; Length 120;  
 Best Local Similarity 30.8%; Pred. No. 8.1e-02; 9; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 9; SEQ ID NO 51  
 LENGTH: 120  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-880-708-20

Query Match 16.6%; Score 26; DB 9; Length 120;  
 Best Local Similarity 30.8%; Pred. No. 8.1e-02; 9; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 9; SEQ ID NO 51  
 LENGTH: 120  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-880-708-20

Query Match 16.6%; Score 26; DB 9; Length 120;  
 Best Local Similarity 30.8%; Pred. No. 8.1e-02; 9; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 9; SEQ ID NO 51  
 LENGTH: 120  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-880-708-20

Query Match 16.6%; Score 26; DB 9; Length 120;  
 Best Local Similarity 30.8%; Pred. No. 8.1e-02; 9; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 9; SEQ ID NO 51  
 LENGTH: 120  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-880-708-20

Query Match 16.6%; Score 26; DB 9; Length 120;  
 Best Local Similarity 30.8%; Pred. No. 8.1e-02; 9; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 9; SEQ ID NO 51  
 LENGTH: 120  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-880-708-20

Query Match 16.6%; Score 26; DB 9; Length 120;  
 Best Local Similarity 30.8%; Pred. No. 8.1e-02; 9; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 9; SEQ ID NO 51  
 LENGTH: 120  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-880-708-20

Query Match 16.6%; Score 26; DB 9; Length 120;  
 Best Local Similarity 30.8%; Pred. No. 8.1e-02; 9; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 9; SEQ ID NO 51  
 LENGTH: 120  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-880-708-20

Query Match 16.6%; Score 26; DB 9; Length 120;  
 Best Local Similarity 30.8%; Pred. No. 8.1e-02; 9; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 9; SEQ ID NO 51  
 LENGTH: 120  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-880-708-20

Query Match 16.6%; Score 26; DB 9; Length 120;  
 Best Local Similarity 30.8%; Pred. No. 8.1e-02; 9; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 9; SEQ ID NO 51  
 LENGTH: 120  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-880-708-20

Query Match 16.6%; Score 26; DB 9; Length 120;  
 Best Local Similarity 30.8%; Pred. No. 8.1e-02; 9; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 9; SEQ ID NO 51  
 LENGTH: 120  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-880-708-20

Query Match 16.6%; Score 26; DB 9; Length 120;  
 Best Local Similarity 30.8%; Pred. No. 8.1e-02; 9; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 9; SEQ ID NO 51  
 LENGTH: 120  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-880-708-20

Query Match 16.6%; Score 26; DB 9; Length 120;  
 Best Local Similarity 30.8%; Pred. No. 8.1e-02; 9; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 9; SEQ ID NO 51  
 LENGTH: 120  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-880-708-20

RESULT 11  
 US-09-813-459-6  
 ; Sequence 6, Application US/09813459  
 ; Patent No. US20020107369A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lee, Se-Jin  
 Cunningham, No. US20020107369A1  
 TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-10  
 NUMBER OF SEQUENCES: 26  
 CORRESPONDENCE ADDRESS:  
 ADDRESSE: Spensley Horn Jubas & Lubitz  
 STREET: 1880 Century Park East, Suite 500  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: USA  
 ZIP: 90067  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/813,459  
 FILING DATE: 20-Mar-2001  
 CLASSIFICATION: <Unknown>  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 08/624,635  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Wetherell, Jr., Ph.D., John R.,  
 REGISTRATION NUMBER: 31,678  
 REFERENCE/DOCKET NUMBER: PD-3054  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619) 455-5100  
 TELEFAX: (619) 455-5110  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
 LENGTH: 120 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 MOLECULE TYPE: protein  
 IMMEDIATE SOURCE:  
 CLONE: GDF-10  
 FEATURE:  
 NAME/KEY: Protein  
 LOCATION: 1..120  
 SEQUENCE DESCRIPTION: SEQ ID NO: 16:  
 US-09-813-459-16  
 Query Match 16.6%; Score 26; DB 10; Length 120;  
 Best Local Similarity 30.8%; Pred. No. 8.1e+02;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
 QY 17 PXXXXXXCGXC 29  
 Db 39 PKSEDAVYCGAC 51  
 RESULT 12  
 US-09-813-459-16  
 Sequence 16, Application US/09813459  
 Patient No. US20020107369A1  
 GENERAL INFORMATION:  
 APPLICANT: Lee, Se-Jin  
 Cunningham, No. US20020107369A1  
 TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-10  
 NUMBER OF SEQUENCES: 26  
 CORRESPONDENCE ADDRESS:  
 ADDRESSE: Spensley Horn Jubas & Lubitz  
 STREET: 1880 Century Park East, Suite 500  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: USA  
 ZIP: 90067  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/813,459  
 FILING DATE: 20-Mar-2001  
 CLASSIFICATION: <Unknown>  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 08/624,635  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Wetherell, Jr., Ph.D., John R.,  
 REGISTRATION NUMBER: 31,678  
 REFERENCE/DOCKET NUMBER: PD-3054  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619) 455-5100  
 TELEFAX: (619) 455-5110  
 INFORMATION FOR SEQ ID NO: 16:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 120 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 MOLECULE TYPE: protein  
 IMMEDIATE SOURCE:  
 CLONE: BMP-3  
 FEATURE:  
 NAME/KEY: Protein  
 LOCATION: 1..120  
 SEQUENCE DESCRIPTION: SEQ ID NO: 16:  
 US-09-995-515-12  
 Query Match 16.6%; Score 26; DB 10; Length 120;  
 Best Local Similarity 30.8%; Pred. No. 8.1e+02;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
 QY 17 PXXXXXXCGXC 29  
 Db 39 PKSEDAVYCGAC 51  
 RESULT 13  
 US-09-995-515-12  
 Sequence 12, Application US/09995515  
 ; Patent No. US2002015169A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Jing, Shuguian  
 ; TITLE OF INVENTION: Transforming Growth Factor-Beta-Related Molecules and  
 ; TITLE OF INVENTION: Uses Thereof  
 ; FILE REFERENCE: 00-659-A  
 ; CURRENT APPLICATION NUMBER: US/09/995,515  
 ; CURRENT FILING DATE: 2001-11-28  
 ; PRIORITY APPLICATION NUMBER: 00/253,476  
 ; PRIORITY FILING DATE: 2000-11-28  
 ; NUMBER OF SEQ ID NOS: 27  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO: 12  
 ; LENGTH: 131  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-995-515-12  
 Query Match 16.6%; Score 26; DB 10; Length 131;  
 Best Local Similarity 30.8%; Pred. No. 8.6e+02;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
 QY 17 PXXXXXXCGXC 29  
 Db 39 PKSEDAVYCGAC 51

Db 103 PKTLSFSYCGTC 115

RESULT 14

US-09-995-515-2

Sequence 2, Application US/09995515

Patent No. US2003151695A1

GENERAL INFORMATION:

APPLICANT: JING, Shiqian

TITLE OF INVENTION: Transforming Growth Factor-Beta-Related Molecules and

FILE REFERENCE: 00-59-A

CURRENT APPLICATION NUMBER: US/09/995, 515

CURRENT FILING DATE: 2001-11-28

PRIOR APPLICATION NUMBER: 60/253, 476

PRIOR FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO: 2

LENGTH: 140

TYPE: PRT

ORGANISM: Homo sapiens

US-09-995-515-2

RESULT 15

US-09-974-879-139

Query Match 16.6%; Score 26; DB 10; Length 140;

Best Local Similarity 30.8%; Pred. No. 9e+02;

Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 17 PXXXXXXXXXGXC 29

Db 153 PTKLTSACIGLC 165

PRIOR APPLICATION NUMBER: US 60/066, 089
PRIOR FILING DATE: 1997-11-17
PRIOR APPLICATION NUMBER: US 60/066, 095
PRIOR FILING DATE: 1997-11-17
PRIOR APPLICATION NUMBER: US 60/066, 090
PRIOR FILING DATE: 1997-11-17
NUMBER OF SEQ ID NOS: 611
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 139
LENGTH: 182
TYPE: PRT
ORGANISM: Homo sapiens

US-09-974-879-139

Query Match 16.6%; Score 26; DB 9; Length 182;
Best Local Similarity 30.8%; Pred. No. 1.1e-03;
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Search completed: March 27, 2003, 11:03:15  
Job time : 14 secs

Publication No. US20030028003A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 125 Human Secreted Proteins
FILE REFERENCE: P2020P2
CURRENT APPLICATION NUMBER: US/09/974, 879
PRIOR APPLICATION NUMBER: US 60/239, 893
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: US 09/818, 683
PRIOR FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: US 09/305, 736
PRIOR FILING DATE: 1999-05-05
PRIOR APPLICATION NUMBER: PCT/US98/23435
PRIOR FILING DATE: 1998-11-04
PRIOR APPLICATION NUMBER: US 60/064, 911
PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: US 60/064, 912
PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: US 60/064, 983
PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: US 60/064, 900
PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: US 60/064, 984
PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: US 60/064, 987
PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: US 60/064, 908
PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: US 60/064, 984
PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: US 60/064, 985
PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: US 60/066, 094
PRIOR FILING DATE: 1997-11-17
PRIOR APPLICATION NUMBER: US 60/066, 100
PRIOR FILING DATE: 1997-11-17

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OM protein - protein search, using sw model

Run on: March 27, 2003, 10:58:19 ; Search time 44 Seconds  
(without alignments)

211.933 Million cell updates/sec

Perfect score: 157

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR: 73;\*

1: pir1;\*  
2: pir2;\*  
3: pir3;\*  
4: pir4;\*

Score. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No. Score Query Length DB ID Description

1 27 17.2 967 2 G86229 hypothetical protein [imported] - *Arabidopsis thaliana* (mouse-ear cress)

2 26 16.6 119 2 S48192 insulin-like growth factor beta-related protein

3 26 16.6 278 2 T20478 hypothetical protein

4 26 16.6 347 2 T24528 hypothetical protein

5 26 16.6 360 2 153032 bone morphogenetic protein

6 26 16.6 470 2 B83991 glycolate oxidase

7 26 16.6 472 1 BMHU3 bone morphogenetic

8 26 16.6 476 2 JC4646 bone morphogenetic

9 26 16.6 478 2 JC4838 probable membrane protein

10 26 16.6 598 2 'I02795 P-glycoprotein - r

11 25 15.9 99 2 S22351 transforming growth factor beta-related protein

12 25 15.9 112 2 A61439 hypothetical protein

13 25 15.9 240 2 T45814 insulin-like growth factor S11 precursor - soybean

14 25 15.9 366 2 T03907 TGF-beta-related protein

15 25 15.9 407 2 HB4920 probable Tub family protein

16 25 15.9 407 2 T37242 transforming growth factor

17 25 15.9 412 2 A39489 transforming growth factor

18 25 15.9 413 1 WFLXLB2 transforming growth factor

19 25 15.9 414 1 WEMKB2 transforming growth factor

20 25 15.9 414 1 WEMSB2 transforming growth factor

21 25 15.9 414 2 A31249 transforming growth factor

22 25 15.9 442 2 B31249 transforming growth factor

23 25 15.9 470 2 D69984 transforming growth factor

24 25 15.9 553 1 A42499 mullerian inhibitory factor

25 25 15.9 555 1 S20100 mullerian inhibitory factor

26 25 15.9 563 2 T20192 hypothetical protein

27 25 15.9 575 1 WFBOM mullerian inhibitory factor

28 25 15.9 575 2 T17153 mullerian inhibitory factor

29 25 15.9 612 2 G83307 hypothetical protein

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Scoring table: BLOSUM62

Gapext 0.5

searched: 283224 seqs, 96134422 residues

RESULTS

RESULT 1

G86229 hypothetical protein [imported] - *Arabidopsis thaliana* (mouse-ear cress)

C;Species: *Arabidopsis thaliana* (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001

C;Accession: G86229

R;Rheologis, A.; Ecker, J.R.; Palm, C.J.; Fedderspiel, N.A.; Kaul, S.; White, O.; Alonso, N.F.; Hughes, B.; Huijar, L. *Nature* 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.-H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Talloker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: G86229

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-667 <S>T>

A;Cross-references: GB:AE005172; NID:93482933; PIDN:AC33218.1; GSPDB:GN00141

C;Genetics:

A;Map position: 1

Query Match Score 17.2%; Score 27; DB 2; Length 967;

Best Local Similarity 30.8%; Pred. No. 1.8e+03;

Matches 4; Conservative 0; Mismatches 9; Index 0; Gaps 0;

QY 17 PXXXXXXXXXCGXC 29

Db 726 PQETRSTRCSGAC 738

RESULT 2

S48192 insulin-like growth factor S11 precursor - soybean

N;Alternate names: leginsulin

C;Species: Glycine max (soybean)

C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 24-Oct-2000

C;Accession: S48192; PN0116

R;Watanabe, Y.; Barashov, S.F.; Komatsu, S.; Hemmings, A.M.; Miyagi, M.; Tsunasawa, S.; Barashov, J.; Bloch, D.; Yamashita, T.; Yamashita, T.; Yamashita, T.

A;Title: A peptide that stimulates phosphorylation of the plant insulin-binding protein

A;Reference number: S48192; MUID:94357216; PMID:8076638

A;Accession: S48192

A;Molecule type: mRNA; protein

A;Residues: 1-119 <WAT>

A;Cross-references: GB:DT17396; NID:9498167; PIDN:BAA04219.1; PID:9498168

R;Barashov, S.F.; Egorov, T.A.

Mol. Biol. (Mosk.) 24, 953-961, 1990

A;Title: Using monoclonal antibodies to insulin for isolating proteins inhibiting cell

ALIGNMENTS

ALIGMENTS

A;Reference number: PN0115; MUID:91066897; PMID:2250683

A;Accession: A00116

A;Molecule type: protein

A;Residues: 20-30; 'M', 32-39 <B&B>

F;1-19/Domain: propeptide #status predicted <PRO>

Query Match 16.6%; Score 26; DB 2; Length 119;

Best Local Similarity 30.8%; Pred. No. 6.9e+02; Mismatches 4; Conservative 4; Matches 4;

Qy 17 PXXXXXXCXC 29

Db 14 PTKEAADCNGAC 26

RESULT 3

T24478

hypothetical protein F01G10.6 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999

C;Accession: T24478

R;Embry. C.

submitted to the EMBL Data Library, October 1996

A;Reference number: 219280

A;Accession: T24478

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Cross-references: EMBL:z81055; PIDN:CAB02894.1; GSPPDB:GN00022; CESP:F01G10.6

A;Experimental source: clone F01G10

A;Genetics:

A;Residues: 1-278 <WIL>

A;Gene: CESP:F01G10.6

A;Map position: 4

A;Introns: 84/1; 168/1

Query Match 16.6%; Score 26; DB 2; Length 278;

Best Local Similarity 30.8%; Pred. No. 1.2e+03; Mismatches 4; Conservative 4; Matches 4; Mismatches 0; Indels 0; Gaps 0;

Qy 17 PXXXXXXCXC 29

Db 59 PSNWFQESC 71

RESULT 4

T24528

hypothetical protein T05E12.1 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999

C;Accession: T24528

R;McMurray, A.

submitted to the EMBL Data Library, November 1996

A;Reference number: 219904

A;Accession: T24528

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-347 <WIL>

A;Cross-references: EMBL:z811585; PIDN:CAB04681.1; GSPPDB:GN00023; CESP:T05E12.1

A;Experimental source: clone T05E12

C;Genetics:

A;Gene: CESP:T05E12.1

A;Map position: 5

A;Introns: 61/3; 90/1; 165/2; 187/3; 256/3

Query Match 16.6%; Score 26; DB 2; Length 347;

Best Local Similarity 30.8%; Pred. No. 1.3e+03; Mismatches 4; Conservative 4; Matches 4; Mismatches 0; Indels 0; Gaps 0;

Qy 17 PXXXXXXCXC 29

Db 69 PRGSCINLACGTC 81

RESULT 5

B3H03

bone morphogenetic protein 3 - rat (fragment)

N;Alternate names: osteogenin

C;Species: *Homo sapiens* (man)

C;Date: 16-Sep-1992 #sequence\_revision 03-Aug-1995

C;Accession: D37278

R;Wozney, J. M.; Rosen, V.; Celeste, A. J.; Mitnick, L. M.; Whitters, M. J.; Kriz, R. W.;

Science 242, 1528-1534, 1988

A;Title: Novel regulators of bone formation: molecular clones and activities.

A;Reference number: A37278; MUID:9972730; PMID:3201241

A;Accession: D37278

A;Molecule type: mRNA

A;Residues: 1-472 <W04>

A;Cross-references: GB:M22491; MUID:9179505; PIDN:AAA51836.1; PMID:9179506

C;Genetics:

A;Gene: GDB:BMPS

Q: Cross-references: GDR:125206; OMIM:112263  
 A: Map position: 4p14-q21  
 C: Superfamily: inibin

C:Keywords: bone; glycoprotein  
 F:1-22/Domain: signal sequence #status predicted <SIG>  
 F:1-23-345/Domain: propeptide #status predicted <PRO>  
 F:117,141,175,220,463/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 16.6%; Score 26; DB 1; Length 472;  
 Best Local Similarity 30.8%; Pred. No. 1.6e+03;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

RESULT 8

QY 17 PXXXXXXCAGXC 29  
 Db 391 PKSFDAVYCSGAC 403

JC4646  
 bone morphogenetic protein-3b precursor - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 10-May-1996 #sequence\_revision 19-Jul-1996 #text\_change 01-Dec-2000  
 C:Accession: JC4646  
 R.Takao, M.; Hino, J.; Takeshita, N.; Konno, Y.; Nishizawa, T.; Matsuo, H.; Kangawa, K.  
 Biochem. Biophys. Res. Commun. 219, 656-662, 1996  
 A:Title: Identification of rat bone morphogenetic protein-3b (BMP-3b), a new member of the  
 A:Reference number: JC4646; MUID:96193707; PMID:8605043  
 A:Accession: JC4646  
 A:Molecule type: mRNA  
 A:Residues: 1-476 <TAK>  
 A:Cross-references: DDBJ:DA9494; NID:9699625; PIDN:BAA08454.1; PID:9699626  
 A:Experimental source: femur  
 C:Comment: This protein plays a role in the central nervous system as well as in new bone  
 C:Superfamily: inibin  
 C:Keywords: bone; glycoprotein  
 F:1-29/Domain: signal sequence #status predicted <PRO>  
 F:30-365/Domain: propeptide #status predicted <MAT>  
 F:367-476/Domain: bone morphogenetic protein-3b #status predicted <MAT>  
 F:114,152,277,467/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 16.6%; Score 26; DB 2; Length 476;  
 Best Local Similarity 30.8%; Pred. No. 1.6e+03;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCAGXC 29  
 Db 395 PKSFDAVYCSGAC 407

RESULT 9

QY 17 PXXXXXXCAGXC 29  
 Db 395 PKSFDAVYCSGAC 407

JC4838  
 bone morphogenetic protein-3b precursor [similarity] - human  
 NCAlternate names: BMP-3b; GDF-10  
 C:Species: Homo sapiens (man)  
 C:Date: 15-Aug-1996 #sequence\_revision 15-Oct-1996 #text\_change 01-Dec-2000  
 C:Accession: JC4838  
 R.Hino, J.; Takao, M.; Takeshita, N.; Konno, Y.; Nishizawa, T.; Matsuo, H.; Kangawa, K.  
 Biochem. Biophys. Res. Commun. 223, 304-310, 1996  
 A:Title: cDNA cloning and genomic structure of human bone morphogenetic protein-3b (BMP-3b)  
 A:Residues: 1-478 <HIN>  
 A:Cross-references: DDBJ:D49492; NID:9699603; PIDN:BAA08452.1; PID:9699604  
 C:Comment: This protein induces endochondral bone formation, chemotaxis of monocytes, and  
 A:Gene: bmp-3b  
 C:Superfamily: inibin  
 C:Keywords: bone  
 F:1-53/Domain: signal sequence #status predicted <SIG>

QY 17 PXXXXXXCAGXC 29  
 Db 397 PKSFDAVYCAAGAC 409

RESULT 10

QY 17 PXXXXXXCAGXC 29  
 Db 397 PKSFDAVYCAAGAC 409

T02795  
 probable membrane protein L549.7 [imported] - Leishmania major (strain Friedlin)  
 C:Species: Leishmania major  
 C:Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 19-May-2000  
 C:Accession: GB1455; T02795  
 R.Myler, P.J.; Audley, L.; Devos, T.; Hixson, G.; Kiser, P.; Lemley, C.; Magness, C.  
 Proc. Natl. Acad. Sci. U.S.A. 96, 2902-2906, 1999  
 A:Title: Leishmania major Friedlin chromosome 1 has an unusual distribution of protein  
 A:Reference number: GB1455; MUID:917887; PMID:10077609  
 A:Accession: GB1455  
 A:Status: Preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-598 <YIL>  
 A:Cross-references: GB:AE001274; NID:93264850; PIDN: AAC24619.1; PID:92978456; GSPPDB:G  
 A:Experimental source: strain MHOM/IL/81/Friedlin  
 C:Genetics: L549.7  
 A:Gene: L549.7  
 A:Map Position: 1  
 C:Superfamily: Leishmania major probable membrane protein L549.7  
 C:Keywords: transmembrane protein

Query Match 16.6%; Score 26; DB 2; Length 598;  
 Best Local Similarity 30.8%; Pred. No. 1.9e+03;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCAGXC 29  
 Db 96 PSSSSGGCGCG 108

RESULT 11

S22351  
 P-glycoprotein - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 05-Nov-1999  
 C:Accession: S22351  
 R.Deuchars, K.L.; Dittie, M.; Ling, V.  
 Biochem. Biophys. Acta 1130, 157-165, 1992  
 A:Title: Identification of distinct P-glycoprotein gene sequences in rat.  
 A:Reference number: S22351; MUID:92223089; PMID:1348630  
 A:Accession: S22351  
 A:Molecule type: DNA  
 A:Residues: 1-99 <DRE>  
 A:Cross-references: EMBL:X61106; NID:956800; PIDN:CAA43418.1; PID:e39738; PID:9133421  
 A:Note: the authors translated the codon TTC for residue 48 as Leu  
 C:Keywords: glycoprotein

Query Match 15.9%; Score 25; DB 2; Length 99;  
 Best Local Similarity 30.8%; Pred. No. 8.8e+02;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCAGXC 29  
 Db 42 PSVTAFLFCGRC 54

RESULT 12

A61439  
 transforming growth factor beta-2 - bovine

N:Alternate names: cartilage-inducing factor B; Mgf-a; milk growth factor a  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 07-oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 07-May-1999  
 C:Accession: A61439; A25485; B42320; S15389  
 R:Jin, Y.; Cox, D.A.; Knecht, R.; Raschdorf, F.; Cerletti, N.  
 J. Protein Chem. 10, 565-575, 1991  
 A:Title: Separation, purification, and sequence identification of TGF-beta1 and TGF-beta2  
 A:Reference number: A61439; MUID:92189724; PMID:1799413  
 A:Accession: A61439  
 A:Molecule type: protein  
 A:Residues: 1-112 <JIN>  
 A:Experimental source: milk  
 R:SEYEDIN, S.M.; SEGARIN, P.R.; ROSEN, D.M.; THOMPSON, A.Y.; BENTZ, H.; GRAYCAR, J.  
 J. Biol. Chem. 262, 1946-1949, 1987  
 A:Title: Cartilage-inducing factor-B is a unique protein structurally and functionally related to the TGF-beta1 and TGF-beta2  
 A:Accession: A25485  
 A:Molecule type: protein  
 A:Residues: 1-30 <SEY>  
 A:Experimental source: bone  
 R:OGAWA, Y.; SCHMIDT, D.K.; DASCH, J.R.; CHANG, R.J.; GLASER, C.B.  
 J. Biol. Chem. 267, 2325-2328, 1992  
 A:Title: Purification and characterization of transforming growth factor-beta2.3 and -beta4  
 A:Accession number: A42320; MUID:92129307; PMID:11733936  
 A:Title: Isolation and characterisation of milk growth factor, a transforming-growth-factor  
 A:Reference number: S15389; MUID:91224126; PMID:2026157  
 A:Accession: S15389  
 A:Molecule type: protein  
 A:Residues: 1-16, XX, 19 <COX>  
 A:Experimental source: milk  
 C:Superfamily: inhibin  
 C:Keywords: growth factor; growth regulation; heterodimer; homodimer  
 Query Match 15.9%; Score 25; DB 2; Length 112;  
 Best Local Similarity 30.8%; Pred. No. 9.6e+02; Mismatches 4; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
 Qy 17 PXXXXXXCGXG 29  
 Db 36 PKGYNANFCAGAC 48

RESULT 13

T45814 hypothetical protein F2809\_210 - *Arabidopsis thaliana* (mouse-ear cress)  
 C:Species: *Arabidopsis thaliana* (mouse-ear cress)  
 C:Accession: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 04-Feb-2000  
 C:Accession: T45814  
 R:Benes, V.; Rechmann, S.; Borkova, D.; Ansgare, W.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.  
 R:Submitted to the Protein Sequence Database, January 2000  
 A:Reference number: Z23014  
 A:Accession: T45814  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-240 <BEN>  
 A:Cross-references: EMBL:All3/080  
 A:Experimental source: cultivar Columbia; BAC clone F2809  
 C:Genetics:  
 A:Map position: 3  
 A:Introns: 38/2; 82/2; 123/2; 196/2  
 A:Note: F2809\_210

Query Match 15.9%; Score 25; DB 2; Length 240;  
 Best Local Similarity 30.8%; Pred. No. 1.5e+03; Mismatches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
 Qy 17 PXXXXXXCGXG 29  
 Db 75 PSRKNVSCAGAC 87

Search completed: March 27, 2003, 11:02:33  
 Job time: 45 secs

Query Match 15.9%; Score 25; DB 2; Length 407;  
 Best Local Similarity 30.8%; Pred. No. 2.1e+03; Mismatches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
 Qy 17 PXXXXXXCGXG 29  
 Db 75 PSRKNVSCAGAC 87

RESULT 14

T03907 TGF-beta-related protein homolog F39G3.8 - *Caenorhabditis elegans*  
 C:Species: *Caenorhabditis elegans*  
 C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 17-Mar-2000  
 C:Accession: T03907  
 R:DU, Z.; LE, T.T.; HOLMES, A.  
 A:Description: The sequence of *C. elegans* cosmid F39G3.  
 A:Reference number: Z15131  
 A:Accession: T03907  
 A:Status: preliminary; translated from GB/EMBL/DDJB  
 A:Molecule type: DNA  
 A:Residues: 1-366 <DUZ>  
 A:Cross-references: EMBL:AF016424; NID:92291203; PIDN:AA65333.1; PID:92291211  
 A:Genetics:  
 A:Map position: V  
 A:Introns: 38/2; 86/2; 110/1; 161/2; 205/1; 229/2; 259/1  
 A:Note: F39G3.8  
 C:Superfamily: inhibin  
 Query Match 15.9%; Score 25; DB 2; Length 366;  
 Best Local Similarity 30.8%; Pred. No. 2e+03; Mismatches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
 Qy 17 PXXXXXXCGXG 29  
 Db 286 PEGFAFYCGDC 298

RESULT 15

H84920 probable Rub family protein [imported] - *Arabidopsis thaliana* (mouse-ear cress)  
 C:Species: *Arabidopsis thaliana* (mouse-ear cress)  
 C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001  
 C:Accession: H84920  
 R;Lin, X.; Kaul, S.; Rounseley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.  
 M.; Koo, H.; Moffat, K.S.; Cionin, L.A.; Shen, M.; VanAken, S.E.; Umapam, L.; Tallon, J.;  
 Neuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, S.  
 Nature 402, 761-768, 1999  
 A:Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.  
 A:Reference number: A84420; MUID:20083487; PMID:10617197  
 A:Accession: H84920  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-407 <STO>  
 A:Cross-references: GB:AE002093; NID:9378302; PIDN: AAC63644.1; GSPDB:GN00139  
 C:Genetics:  
 A:Gene: At2g47900  
 A:Map position: 2

Query Match 15.9%; Score 25; DB 2; Length 407;  
 Best Local Similarity 30.8%; Pred. No. 2.1e+03; Mismatches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
 Qy 17 PXXXXXXCGXG 29  
 Db 75 PSRKNVSCAGAC 87

Search completed: March 27, 2003, 11:02:33  
 Job time: 45 secs

Query Match 15.9%; Score 25; DB 2; Length 240;  
 Best Local Similarity 30.8%; Pred. No. 1.5e+03; Mismatches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
 Qy 17 PXXXXXXCGXG 29



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CC

DR

EMBL: AE042381; AAC30334.1; -;

DR TIGR0111; mtrA; 1; -;

DR TRANSFERASE; Methyldtransferase; Methanogenesis; cobalt.

FT BINDING 85 85 5-HYDROXYBENZIMIDAZOL COBAMIDE COFACTOR (BY SIMILARITY).

FT DOMAIN 169 176 POLY-LHU.

FT DOMAIN 232 238 POLY-GLU.

FT CONFLICT 16 16 G -> R (IN REF. 1).

FT CONFLICT 71 71 N -> D (IN REF. 1).

FT CONFLICT 127 127 E -> G (IN REF. 1).

FT CONFLICT 161 161 D -> E (IN REF. 1).

SQ SEQUENCE 240 AA; 25366 MW; 44C086DD3561E526 CRC64;

RESULT 2

Query Match 17.2%; Score 27; DB 1; Length 240; Best Local Similarity 30.8%; Pred. No. 2.3e+02; Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0; RN

QY 17 PXXXXXXCGXC 29

Db 40 PILDAGAACTGSC 52

RESULT 3

ALBL\_SOYBN STANDARD; PRM; 119 AA.

ID ALBL\_SOYBN

AC Q39837; O49854;

DT 16-OCT-2001 (Rel. 40, last sequence update)

DT 16-OCT-2001 (Rel. 40, last annotation update)

DE Albumin 1 precursor (PA1) (contains: PA1A; Leginsulin (PA1B)).

OS Glycine max (soybean).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

OC NCBI\_TaxID=3847;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CV; Miyagishiro;

RC STRAIN=CV; Miyagishiro; TISSUE=Radicle;

RC MEDLINE=94357216; PubMed=8076638;

RA Watanabe Y.; Barashov S.F.; Komatsu S.; Hemmings A.M.; Miyagi M.; Tsunawa S.; Hirano H.

RA "A peptide that stimulates phosphorylation of the plant insulin-binding protein. Isolation, primary structure and cDNA cloning.";

RL Eur. J. Biochem. 224:167-172(1994).

RN [2]

RP SEQUENCE FROM N.A.

RA STRAIN=CV; Miyagishiro;

RA Tan J.Z.; Lou C.F.; Hirano H.;

RT "Analysis of leginsulin gene in soybean cultivar (Glycine max) and wild species (Glycine soja).";

RT wild species (Glycine soja);

RT Chin. J. Appl. Environ. Biol. 5:259-263(1999).

RL Chin. J. Appl. Environ. Biol. 5:259-263(1999).

RN [3]

RP REVISION TO 64.

RC STRAIN=CV; Miyagishiro;

RA Hirano H.;

CC Submitted (JUN-2001) to the SWISS-PROT data bank.

-I- FUNCTION: LEGINSULIN Binds to BASIC 7S GLOBULIN (BG) AND STIMULATES ITS PHOSPHORYLATION ACTIVITY. INVOLVED IN THE SIGNAL TRANSDUCTION SYSTEM TO REGULATE THE GROWTH AND DIFFERENTIATION AS A HORMONE PEPTIDE.

CC -I- PTM: THREE DISULFIDE BONDS ARE PROBABLY PRESENT IN LEGINSULIN.

CC -I- PTM: THE C-TERMINAL GLYCINE MAY BE REMOVED FROM LEGINSULIN.

CC

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CC

DR EMBL: AJ011935; CAA09880.2; -;

DR EMBL: AJ223037; CAA11040.1; -;

DR Seed storage protein; Albumin; Signal.

FT SIGNAL 1 19 LEGINSULIN.

FT CHAIN 20 56 POTENTIAL.

FT PROPER 57 64 PALA (POTENTIAL).

FT CHAIN 65 116 PALA (POTENTIAL).

FT PROPER 117 119 POTENTIAL.

SQ SEQUENCE 119 AA; 13046 MW; A054491D7BE1AA70 CRC64;

Query Match 16.6%; Score 26; DB 1; Length 119; Best Local Similarity 30.8%; Pred. No. 2.1e+02; Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0; RN

QY 17 PXXXXXXCGXC 29

Db 14 PTKEAADCNGAC 26

RESULT 4

Y816_DRONE		STANDARD;		PRT;	355 AA.
ID	Q9FA0;				
AC					
DT	16-OCT-2001 (Rel. 40, Created)				
DT	16-OCT-2001 (Rel. 40, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	Hypothetical protein CG7816.				
GN	CG7816.				
OS	Drosophila melanogaster (Fruit fly).				
OC	Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;				
OC	Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;				
OC	Muscomorpha; Ephydriodea; Drosophilidae; Drosophila.				
OX	NCBI_TAXID=227;				
RN	[1] SEQUENCE FROM N.A.				
RP	SEQUENCE FROM N.A.				
RX	STRAIN=Berkeley;				
RC	MEDLINE=2016006; PubMed=10731132;				
RA	Adams M.D., Ceolniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,				
RA	Amannette P.G., Scheerer S.E., Li P.W., Hoskins R.A., Galle R.F.,				
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RA	Zheng X.H., Zhong F.N., Zhou W., Zhou X., Zhu S., Zhu X., Smith H.O.,				
RA	Glibbs A.A., Myers E.W., Rubin G.M., Venter J.C.;				
RT	"The genome sequence of <i>Drosophila melanogaster</i> ;"				
RL	Science 287:2185-2195 (2000).				
CC	-- SUBCELLULAR LOCATION: Integral membrane protein (Probable).				
CC	-- SIMILARITY: BELONGS TO THE KE4/CATSUP FAMILY.				
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CC	EMBL; AR03771; ARN56960.1.-.				
DR	FlyBase; FBgn039114; CG7816.				
DR	InterPro; IPR003659; Zn_trprrt_zip.				
DR	PFam; PF02535; ZBP; 1.				
KW	Hypothetical protein; Transmembrane; Glycoprotein.				
FT	TRANSMEM 37 57 POTENTIAL.				
TRANSMEM	79 99 POTENTIAL.				
FT	SEQUENCE FROM N.A.				
RX	STRAIN=Berkeley;				
RC	MEDLINE=2016006; PubMed=10731132;				
RA	Adams M.D., Ceolniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,				
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TRANSMEM	79 99 POTENTIAL.				
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RA	Glibbs A.A., Myers E.W., Rubin G.M., Venter J.C.;				
RT	"The genome sequence of <i				

Query Match 16.6%; Score 26; DB 1; Length 468;  
Best Local Similarity 30.8%; Pred. No. 5.3e+02; 0; Mismatches 9; Indels 0; Gaps 0;  
Matches 4;

OY 17 PXXXXXXCXC 29  
Db 387 PRSFDAYCSCAC 399

Query Match 16.6%; Score 26; DB 1; Length 472;  
Best Local Similarity 30.8%; Pred. No. 5.4e+02; 0; Mismatches 9; Indels 0; Gaps 0;  
Matches 4;

OY 17 PXXXXXXCXC 29  
Db 391 PKSFDAYCCGAC 403

Query Match 16.6%; Score 26; DB 1; Length 468;  
Best Local Similarity 30.8%; Pred. No. 5.3e+02; 0; Mismatches 9; Indels 0; Gaps 0;  
Matches 4;

OY 17 PXXXXXXCXC 29  
Db 387 PRSFDAYCSCAC 399

Query Match 16.6%; Score 26; DB 1; Length 472;  
Best Local Similarity 30.8%; Pred. No. 5.4e+02; 0; Mismatches 9; Indels 0; Gaps 0;  
Matches 4;

OY 17 PXXXXXXCXC 29  
Db 391 PKSFDAYCCGAC 403

Query Match 16.6%; Score 26; DB 1; Length 472;  
Best Local Similarity 30.8%; Pred. No. 5.4e+02; 0; Mismatches 9; Indels 0; Gaps 0;  
Matches 4;

OY 17 PXXXXXXCXC 29  
Db 391 PKSFDAYCCGAC 403

RESULT 6

BM3\_HUMAN STANDARD; PRT; 472 AA.

AC P12645; DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-OCT-1989 (Rel. 12, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Bone morphogenetic protein 3 precursor (BMP-3)  
GN BMP3.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
OX NCBI\_TAXID=9606;  
RN [1]  
RX MEDLINE=89072730; PubMed=3201241;  
RA Wozney J.M., Rosen V., Celeste J.A., Mitschok L.M., Whitters M.J.,  
RA Kriz R.W., Hewick R.M., Wang E.A.;  
RT "Novel regulators of bone formation: molecular clones and  
RT activities";  
RL Science 243:1520-1534(1988).  
CC -1 FUNCTION: INDUCES CARTILAGE AND BONE FORMATION  
CC -1 SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).  
CC -1 TISSUE SPECIFICITY: EXPRESSED IN LUNG, OVARY AND SMALL INTESTINE.  
CC -1 SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

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CC

DR EMBL; M22491; AAA51836.1; -.  
DR PIR; D37228; D37228.  
DR HSSP; P12643; 3BMP.  
DR GeneW; HGNC;1:070; BMP3.  
DR MIM; 112263; -.  
DR InterPro; IPR002400; GF\_CYSKNOT.  
DR InterPro; IPR001839; TGFB.  
DR Pfam; PF00019; TGF-beta; 1.  
DR ProDom; PDD00357; TGFB; 1.  
DR SMART; SM00204; TGFB; 1.  
DR PROSITE; PS00250; TGF\_BETA; 1.  
DR SIGNAL; Growth factor; Cytokine; Glycoprotein.  
FT SIGNAL; 1 22 POTENTIAL.  
FT PROPEP 23 362 POTENTIAL.  
FT CHAIN 363 472 BONE MORPHOGENETIC PROTEIN 3.  
FT DISULFD 370 437 BY SIMILARITY.  
FT DISULFD 370 437 BY SIMILARITY.  
FT DISULFD 399 469 BY SIMILARITY.

FT CARBOHYD 139 139 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 171 171 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 216 216 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 459 459 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 468 AA; 52675 MW; 05315D4954DC3CA1 CRC64;

RESULT 6

BM3\_MOUSE STANDARD; PRT; 472 AA.

AC P97737; DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Bone morphogenetic protein 3b precursor (BMP-3b)  
DE (Growth/differentiation factor 10) (GDF-10).  
GN GDF10 OR BMPB.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TAXID=10090;  
RN [1]  
SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.  
RC STRAIN=CD-1; TISSUE=Uterus;  
RX MEDLINE=96115614; PubMed=8679252;  
RA Cunningham N.S., Jenkins N.A., Gilbert D.J., Copeland N.G.,  
RA Redell A.H., Lee S.-J.;  
RT "Growth/differentiation factor-10: a new member of the transforming  
RT growth factor-beta superfamily related to bone morphogenetic  
RT protein 3.";  
RL Growth Factors 12:99-109(1995).  
CC -1 SUBUNIT: HOMODIMER OR HETERO DIMER (POTENTIAL).  
CC -1 TISSUE SPECIFICITY: Expressed in uterus, adipose tissue, brain and  
CC bone, and to a lesser extent in liver and spleen.  
CC -1 SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

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CC or send an email to licensee@isb-sib.ch).

CC

DR EMBL; S82648; AAB46753.1; -.  
DR HSSP; P12643; 3BMP.  
DR MGP; MGT; 95584; Gdf10.  
DR InterPro; IPR001839; TGFB.  
DR Pfam; PF00019; TGF-beta; 1.  
DR ProDom; PDD00357; TGFB; 1.  
DR SMART; SM00204; TGFB; 1.  
DR PROSITE; PS00250; TGF\_BETA; 1.  
FT SIGNAL; 1 29 POTENTIAL.  
FT PROPEP 30 366 BONE MORPHOGENETIC PROTEIN 3B.  
FT CHAIN 367 475  
FT DISULFD 374 441 BY SIMILARITY.  
FT DISULFD 403 473 BY SIMILARITY.  
FT DISULFD 407 475 BY SIMILARITY.  
FT DISULFD 440 440 BY SIMILARITY.  
FT CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).





FT CHAIN 261 399 BONE MORPHOGENETIC PROTEIN 8B.  
 FT DISULFID 298 364 BY SIMILARITY.  
 FT DISULFID 327 396 BY SIMILARITY.  
 FT DISULFID 331 398 BY SIMILARITY.  
 FT DISULFID 363 363 INTERCHAIN (BY SIMILARITY).  
 FT CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 340 340 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 399 AA; 44752 MW; EFA0B78C7EC4839 CRC64;  
 Query Match 15.9%; Score 25; DB 1; Length 399;  
 Best Local Similarity 30.8%; Pred. No. 6.9e+02; 0; Mismatches 9; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
 Qy 17 PXXXXXXCGXGC 29  
 Db 319 PGGYSAYTCAGBC 331

RESULT 12

ID TGF2\_CHICK STANDARD; PRT; 412 AA.

AC P30371; 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DE Transforming growth factor beta 2 precursor (TGF-beta 2).  
 GN TGBB2.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauvia; Aves; Neognathae; Galliformes; Phasianidae;  
 OC Gallus.  
 RA Burt D.W., Paton J.R.;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN="White leghorn"; TISSUE=Blood;  
 RX MEDLINE=92075163; PubMed=1683775;

RT "Molecular cloning and primary structure of the chicken transforming growth factor-beta 2 gene.,"  
 RL DNA Cell Biol. 10:723-734(1991).

CC -1- FUNCTION: TGF-BETA 2 HAS SUPPRESSIVE EFFECTS ON INTERLEUKIN-2 DEPENDENT T-CELL GROWTH.  
 -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.  
 -1- SUBCELLULAR LOCATION: secreted.

CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

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CC EMBL; X58071; CAA41101.1; -  
 EMBL; X59082; CAA41101.1; JOINED.  
 EMBL; X59081; CAA41101.1; JOINED.  
 EMBL; X59080; CAA41101.1; JOINED.  
 PIR; A39489; A39489.

DR HSSP; P08112; 20GI.  
 DR InterPro; IPR002400; GF\_CYSKNOT.  
 DR InterPro; IPR002431; TGF\_TGFb.  
 DR InterPro; IPR001839; TGFB.  
 DR InterPro; IPR001111; TGFB\_N.  
 DR Pfam; PF00688; TGFb\_propeptide; 1.  
 DR PRINTS; PRO0438; GRCISKNOT.  
 DR PRINTS; PRO1423; TGFbeta.  
 DR PRODOM; PDD00357; TGFB; 1.  
 DR SMART; SM00204; TGFB; 1.  
 DR PROSITE; PS00250; TGF\_BETA\_1; 1.  
 KW Growth factor; Mitogen; Glycoprotein; Signal.

FT SIGNAL 1 20 POTENTIAL.

FT PROPEP 21 300 TRANSFORMING GROWTH FACTOR BETA 2.  
 FT CHAIN 301 412 BY SIMILARITY.  
 FT DISULFID 307 316 BY SIMILARITY.  
 FT DISULFID 315 378 BY SIMILARITY.  
 FT DISULFID 344 409 BY SIMILARITY.  
 FT DISULFID 348 411 BY SIMILARITY.  
 FT DISULFID 377 377 INTERCHAIN (BY SIMILARITY).  
 FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 139 139 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 412 AA; 47606 MW; 93E759BF1BD958DC CRC64;  
 Query Match 15.9%; Score 25; DB 1; Length 412;  
 Best Local Similarity 30.8%; Pred. No. 7.1e+02; 0; Mismatches 9; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
 Qy 17 PXXXXXXCGXGC 29  
 Db 336 PKGYHANFCAGAC 348

RESULT 13

ID TGF2\_XENLA STANDARD; PRT; 413 AA.

AC P17247; 01-ANL-1990 (Rel. 15, Created)  
 DT 01-ANL-1990 (Rel. 15, Last sequence update)  
 DE Transforming growth factor beta 2 precursor (TGF-beta 2).  
 GN TGBB2.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;  
 OC Xenopodinae; Xenopus.  
 RA NCBI\_TAXID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92045678; PubMed=2336403;  
 RA Rebboh M.I., Bhatia-Dey N., David I.B.;  
 RT "The sequence of TGF-beta 2 from *Xenopus laevis*."  
 RL Nucleic Acids Res. 18:2185-2185 (1990).  
 CC -1- FUNCTION: TGF-BETA 2 HAS SUPPRESSIVE EFFECTS ON INTERLEUKIN-2 DEPENDENT T-CELL GROWTH.  
 CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.  
 CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

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CC EMBL; X5817; CAA36116.1; -  
 DR EMBL; X5817; CAA36117.1; ALN\_INIT.  
 DR PIR; S09510.  
 DR HSSP; P08112; 20GI.  
 DR InterPro; IPR002400; GF\_CYSKNOT.  
 DR InterPro; IPR003911; TGF\_TGFb.  
 DR InterPro; IPR001839; TGFB.  
 DR InterPro; IPR001111; TGFB\_N.  
 DR Pfam; PF00019; TGF-beta; 1.  
 DR PRINTS; PRO0438; GRCISKNOT.  
 DR PRINTS; PRO1423; TGFbeta.  
 DR PRODOM; PDD00357; TGFB; 1.  
 DR SMART; SM00204; TGFB; 1.  
 DR PROSITE; PS00250; TGF\_BETA\_1; 1.  
 KW Signal; Mitogen; Glycoprotein; Growth factor.  
 FT SIGNAL 1 19 POTENTIAL.

FT PROPERP 20 301

FT CHAIN 302 413 TRANSFORMING GROWTH FACTOR BETA 2.  
 FT DISULFD 308 317 BY SIMILARITY.  
 FT DISULFD 316 379 BY SIMILARITY.  
 FT DISULFD 345 410 BY SIMILARITY.  
 FT DISULFD 349 412 BY SIMILARITY.  
 FT DISULFD 378 378 INTERCHAIN (BY SIMILARITY).  
 FT CARBOHD 72 72 N-LINED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHD 140 140 N-LINED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHD 241 241 N-LINED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 413 AA; 47639 MW; 612715B38734010 CRC64;

Query Match 15.9%; Score 25; DB 1; Length 413;  
 Best Local Similarity 30.8%; Pred. No. 7.1e+02; DB Matches 4;  
 Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
 Oy 17 PRXXXXXXCXCX 29  
 Db 337 PRGYNANFCAGAC 349

RESULT 14  
 TGF2\_HUMAN STANDARD;  
 AC P08112; Q13579; Q15561;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-AUG-1988 (Rel. 08, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Transforming growth factor beta 2 precursor (TGF-beta 2)  
 DE (Glioblastoma-derived T-cell suppressor factor) (G-TSF) (BSC-1 cell  
 DE growth inhibitor) (Polyargin) (Ceteromim).  
 GN TGF2B2.  
 OS Homo sapiens (Human), and  
 OS Cercopithecus aethiops (Green monkey) (Grivet).  
 OC Bukaryota; Metazoa; Chorata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TAXID=9606, 9534;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM A).  
 RC SPECIES=Human;  
 RX MEDLINE=88111555; PubMed=3322013;  
 RA de Martin R., Haendler B., Hofer-Warbinek R., Gaugitsch H., Wrann M.,  
 RA Schluener H., Seifert J.M., Bodmer S., Fontana A., Hofer E.,  
 RT "Complementary DNA for human glioblastoma-derived T cell suppressor  
 RT factor, a novel member of the transforming growth factor-beta gene  
 RT family." 6:3673-3677(1987).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM B).  
 RC SPECIES=Human;  
 RX MEDLINE=88166349; PubMed=3162414;  
 RA Madisen L., Webb N.R., Rose T.M., Marquardt H., Ikeda T.,  
 RA Twardzik D.R., Seyedin S., Purchio A.F.;  
 RT "Transforming growth factor-beta 2: cDNA cloning and sequence  
 RT analysis";  
 RL DNA 7:1-8(1988).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORMS A AND B).  
 RC SPECIES=Human;  
 RX MEDLINE=89090808; PubMed=2850146;  
 RA Webb N.R., Madisen L., Rose T.M., Purchio A.F.;  
 RT "Structural and sequence analysis of TGF-beta 2 cDNA clones predicts  
 RT two different precursor proteins produced by alternative mRNA  
 RT splicing";  
 RL DNA 7:493-497(1988).  
 [4]  
 RP SEQUENCE FROM N.A. (ISOFORM A).  
 RC SPECIES=C.elegans;  
 RX MEDLINE=88124824; PubMed=3277172;  
 RA Hanks S., Armour R., Baldwin J.H., Maldonado F., Spiess J.,  
 RA Holley R.W.;  
 RT "Amino acid sequence of the BSC-1 cell growth inhibitor (polyargin)  
 RT deduced from the nucleotide sequence of the cDNA";  
 PROC. NATL. ACAD. SCI. U.S.A. 85:79-82(1988).  
 RL

RN [5]  
 RP SEQUENCE OF 1-115 FROM N.A.  
 RC SPECIES=Human; TISSUE="lung";  
 RX MEDLINE=92110032; PubMed=1764261;  
 RA Noma T., Glick A.B., Geiser A.G., O'Reilly M.A., Miller J.,  
 RA Roberts A.B., Sporn M.B.;  
 RT "Molecular cloning and structure of the human transforming growth  
 factor-beta 2 gene promoter." RT  
 RT Growth Factors 4:247-255(1991).  
 RL [6]  
 RN SEQUENCE OF 303-414.  
 RC SPECIES=Human;  
 RX MEDLINE=87308213; PubMed=3476488;  
 RA Marquardt H., Lioubin M.N., Ikeda T.;  
 RT "Complete amino acid sequence of human transforming growth factor-  
 type beta 2"; RT  
 RT J. Biol. Chem. 262:12127-12131(1987).  
 RL [7]  
 RN X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).  
 RA MEDLINE=9235881; PubMed=1631557;  
 RA Daquin S., Piez K.A., Ogawa Y., Davies D.R.;  
 RT "Crystal structure of transforming growth factor-beta 2: an unusual  
 RT fold for the superfamily";  
 RL Science 257:369-373(1992).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).  
 RX MEDLINE=92350287; PubMed=1641027;  
 RA Schluener M.P., Gruetter M.G.;  
 RT "An unusual feature revealed by the crystal structure at 2.2-A  
 resolution of human transforming growth factor-beta 2";  
 RL Nature 358:430-434(1992).  
 RN [9]  
 RP VARIANT HIS 91.  
 RX MEDLINE=21419167; PubMed=11528528;  
 RA Alansari A., Haider A.H., Bayat A., Eyré S., Carthy D., Ollier W.E.;  
 RT "Two novel polymorphisms in the human transforming growth factor  
 beta 2 gene." RT  
 RL Genes Immun. 2:295-296(2001).  
 CC -1- FUNCTION: TGF-BETA 2 HAS SUPPRESSIVE EFFECTS ON INTERLEUKIN-2  
 CC - DEPENDENT T-CELL GROWTH.  
 RA -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A (SHOWN HERE) AND B; ARE  
 CC - PRODUCED BY ALTERNATIVE SPLICING. ISOFORM B IS ENCODED BY A MINOR  
 CC - 5.1 KB mRNA SPECIES PRESENT IN HUMAN AND SIMIAN CELLS.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
 CC  
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 CC  
 DR EMBL; Y00083; CAAG68279; 1; -.  
 DR EMBL; M19154; AAAG50404; 1; -.  
 DR EMBL; M19154; AAAG50405; 1; ALT\_SEQ.  
 DR EMBL; J03585; AAAG3538; 1; -.  
 DR EMBL; M87843; AAAG61162; 1; -.  
 DR PIR; S06216; S06216.  
 DR PIR; A29478; A29478.  
 DR PIR; A29798; A29798.  
 DR PIR; A34005; A34005.  
 DR PDB; 1TFG; 31-OCT-93.  
 DR PDB; 2TGI; 31-JAN-94.  
 DR Genew; HGNC:11768; TGF2B2.  
 DR MM:190220; -.  
 DR InterPro; IPR02400; GF\_cysknob.  
 DR InterPro; IPR003911; TGF\_TGFb.  
 DR InterPro; IPR001839; TGFb.  
 DR InterPro; IPR00111; TGFb\_1.  
 DR Pfam; PF00019; TGF-beta; 1.

DR Pfam; PRO0688; TGFb\_propeptide; 1.  
 DR PRINS; PRO038; GFCYKNOT.  
 DR PRINS; PRO123; TGFbTA.  
 DR PROBOM; PRO0157; TGFb; 1.  
 DR SMART; SM0204; TGFb; 1.  
 DR PROSITE; PS00250; TGF\_beta\_1; 1.  
 DR Growth factor; Mitogen; Glycoprotein; Signal; Alternative splicing;  
 KW 3D-structure.  
 FT SIGNAL 1 19 POTENTIAL.  
 FT PROPER 20 302 TRANSFORMING GROWTH FACTOR BETA 2.  
 FT CHAIN 303 414  
 FT DISULFID 309 318  
 FT DISULFID 317 380  
 FT DISULFID 346 411  
 FT DISULFID 413  
 FT CARBOHYD 72  
 FT CARBOHYD 140  
 FT CARBOHYD 241  
 FT CARBOHYD 116  
 FT VARSPLIC 350  
 FT VARIANT 91 91  
 FT CONFLICT 32 32  
 FT HELIX 306 309  
 FT TURN 310 311  
 FT STRAND 316 316  
 FT STRAND 318 320  
 FT STRAND 323  
 FT HELIX 326  
 FT TURN 333 334  
 FT STRAND 335 337  
 FT STRAND 340 342  
 FT STRAND 345 347  
 FT STRAND 349  
 FT TURN 352 353  
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 FT STRAND 380  
 FT STRAND 385  
 FT TURN 395  
 FT STRAND 397  
 FT STRAND 411  
 SQ SEQUENCE 414 AA; 47747 MW; 7D9D569P0FA407D0 CRC64;

Query Match 15.9%; Score 25; DB 1; Length 414;  
 Best Local Similarity 30.8%; Pred. No. 7.1e-02;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCGXC 29  
 Db 338 PKGYNANFCAGAC 350

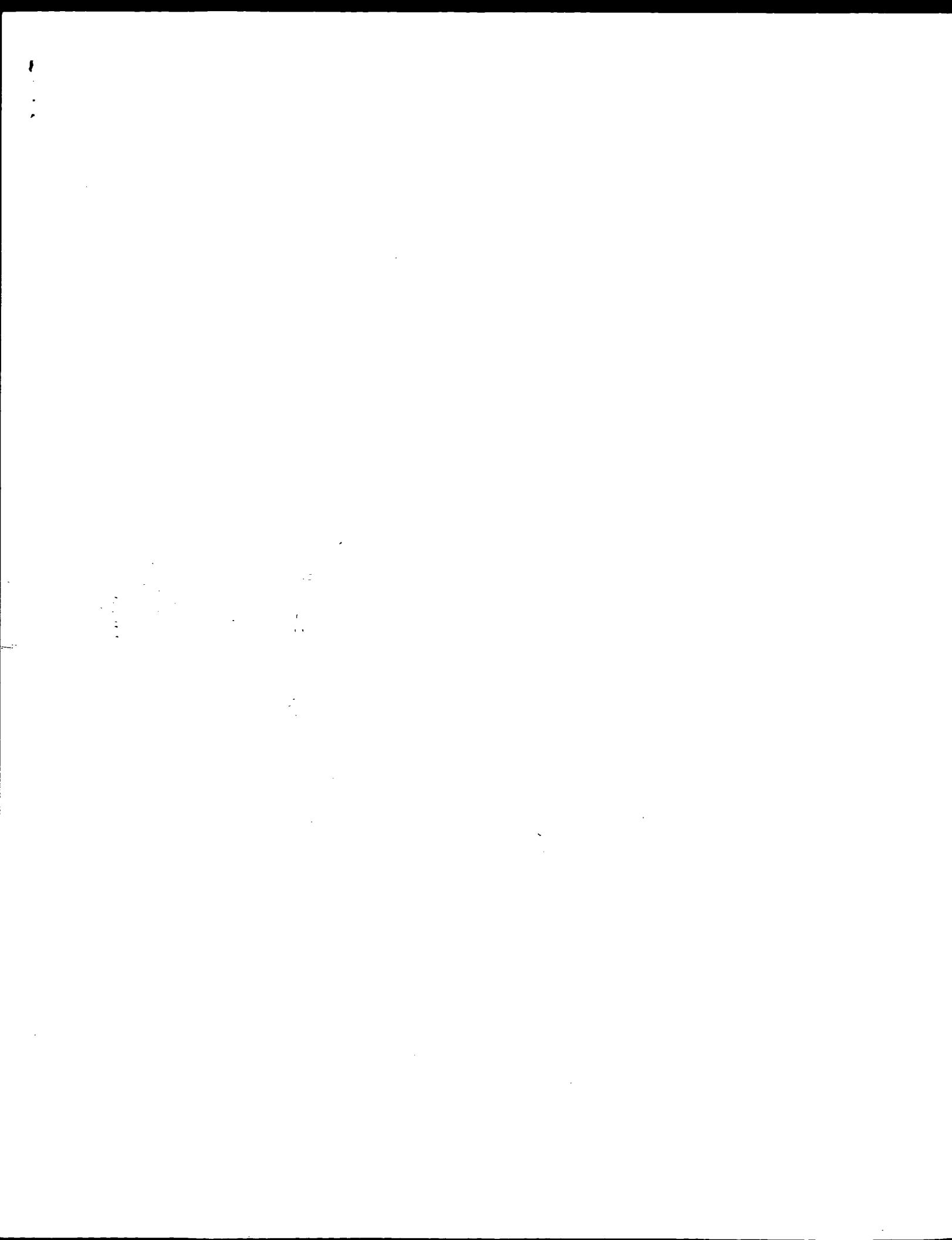
RESULT 15  
 TGF2\_MOUSE  
 ID TGF2\_MOUSE STANDARD; PRT; 414 AA.  
 AC P27050;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-AUG-1992 (Rel. 23, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Transforming growth factor beta 2 precursor (TGF-beta 2).  
 GN TGFb2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; MUS.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 SEQUENCE FROM N.A.  
 RP MEDLINE=90014832; PubMed=2797004;  
 RX Miller D.A., Lee A., Pelton R.W., Chen E.Y., Moses H.L.,  
 RA Deryck R.;

RT "Murine transforming growth factor-beta 2 cDNA sequence and  
 RT expression in adult tissues and embryos.";  
 RL Mol. Endocrinol. 3:1108-1114 (1989).  
 CC -1- FUNCTION: TGF-BETA 2 HAS SUPPRESSIVE EFFECTS ON INTERLEUKIN-2  
 CC DEPENDENT T-CELL GROWTH.  
 CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
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 CC  
 DR EMBL; X57413; CAA0672.1; -.  
 DR PIR; AA0148; WFM5B2.  
 DR HSSP; P08112; 2GCI.  
 DR MGI; 98726; TGFb2.  
 DR InterPro; IPR002400; GF\_cysknot.  
 DR InterPro; IPR00911; TGF\_beta.  
 DR InterPro; IPR00839; TGFb.  
 DR InterPro; IPR00111; TGFb\_N.  
 DR InterPro; IPR00119; TGF\_beta\_1.  
 DR InterPro; IPR00911; TGF\_beta.  
 DR InterPro; IPR00839; TGFb.  
 DR PRINS; PRO00438; GFCYKNOT.  
 DR PRINS; PRO1423; TGFbTA.  
 DR PRODOM; PD000357; TGFb.  
 DR SMART; SM00204; TGFb; 1.  
 DR PROSITE; PS00250; TGF\_beta\_1; 1.  
 KW Growth factor; Mitogen; Glycoprotein; Signal.  
 FT SIGNAL 1 19 POTENTIAL.  
 FT PROPER 20 302 TRANSFORMING GROWTH FACTOR BETA 2.  
 FT CHAIN 303 414  
 FT DISULFID 309 318  
 FT DISULFID 317 380  
 FT DISULFID 346 411  
 FT DISULFID 350 413  
 FT DISULFID 379 379  
 FT CARBOHYD 72 72  
 FT CARBOHYD 140 140  
 FT CARBOHYD 241 241  
 SQ SEQUENCE 414 AA; 47601 MW; 449BC6FA22087FB6 CRC64;

Query Match 15.9%; Score 25; DB 1; Length 414;  
 Best Local Similarity 30.8%; Pred. No. 7.1e+02;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCGXC 29  
 Db 338 PKGYNANFCAGAC 350

Search completed: March 27, 2003, 11:00:10  
 Job time : 26 secs



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OM protein - protein search, using sw model

Run on: March 27, 2003, 10:57:09 ; Search time 85 Seconds

(without alignments)  
235.136 Million cell updates/sec

Title: US-09-828-607-6

Perfect score: 157

Sequence: 1 XXXXXXXXXXXXXXXXXX 97

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs., 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%, Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL\_21:\*

1: sp\_archea:\*

2: sp\_bacteria:\*

3: sp\_fungi:\*

4: sp\_human:\*

5: sp\_invertebrate:\*

6: sp\_mammal:\*

7: sp\_mhc:\*

8: sp\_organelle:\*

9: sp\_phage:\*

10: sp\_plant:\*

11: sp\_rabbit:\*

12: sp\_virus:\*

13: sp\_vertebrate:\*

14: sp\_unclassified:\*

15: sp\_rvirus:\*

16: sp\_bacterioplasm:\*

17: sp\_archeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No. Score Query Match Length DB ID Description

1 27 17.2 102 11 Q9P7Q2 09d7q2 mus musculus

2 27 17.2 549 3 Q9Y754 09y754 emericella

3 27 17.2 967 10 Q80540 arabidopsis

4 26 16.6 87 13 Q42306 carassius a

5 26 16.6 230 2 Q9Z4A9 09z4a9 shigella so

6 26 16.6 230 2 Q9R2H2 09r2h2 salmonella

7 26 16.6 240 10 Q9SDK7 09sdk7 oryza sativ

8 26 16.6 257 4 Q9HTT3 09htt3 homo sapiens

9 26 16.6 278 5 Q17764 017764 caenorhabdi

10 26 16.6 347 5 Q18027 018027 caenorhabdi

11 26 16.6 349 11 Q8R209 08r209 mus musculus

12 26 16.6 366 13 Q9DFC6 09dfc6 xenopus lae

13 26 16.6 367 13 Q9DD36 09dd36 xenopus lae

14 26 16.6 367 13 Q9PRC5 09prc5 xenopus lae

15 26 16.6 376 13 Q9PTQ2 09ptq2 cyprinus ca

17 26 16.6 428 5 Q16134 016134 brugia malae

18 26 16.6 440 6 Q9GLC6 09glc6 rangifer ta

19 26 16.6 470 16 Q9K9B9 09k9b9 bacillus ha

20 26 16.6 598 5 Q9XZ62 09xz62 drosophila

21 26 16.6 598 5 Q60968 leishmania

22 26 16.6 598 5 Q9V4F4 09v4f4 drosphebia

23 25 15.9 62 13 Q9DP5 09dp5 scophthalmus

24 25 15.9 62 13 Q92J7 092j7 anguilla an

25 25 15.9 62 13 Q90F4 090f4 oncorhynchus

26 25 15.9 77 13 Q9YF8 09yf8 oncorhynchus

27 25 15.9 86 6 Q28241 028241 cervus elaphus

28 25 15.9 88 13 Q90F7 090f7 oncorhynchus

29 25 15.9 88 13 Q9YF5 09yf5 pleuroectes

30 25 15.9 91 6 Q9M7Z1 09m7z1 capra hircus

31 25 15.9 99 11 Q63405 063405 rattus norvegicus

32 25 15.9 116 12 Q9TJ1 09tj1 tupaias hebe

33 25 15.9 150 12 Q9Q1U6 09q1u6 saimiriinae

34 25 15.9 200 13 Q9QYF1 09qyf1 pleuroectes

35 25 15.9 240 10 Q9M7L 09m7l

36 25 15.9 255 11 Q92J1 092j1 mus musculus

37 25 15.9 320 13 Q9P0K3 09p0k3 galago senegalensis

38 25 15.9 329 13 Q985Q0 098sq0 melaleuca gummifera

39 25 15.9 352 13 Q9D63 09d63 oncorhynchus

40 25 15.9 361 13 Q98B54 098b54 cyprinus carpio

41 25 15.9 362 13 Q9PVN4 09pvn4 galulus gallus

42 25 15.9 362 13 Q9W617 09w617 brachydanius

43 25 15.9 366 5 Q16273 016273 caenorhabditis elegans

44 25 15.9 372 5 Q9SYK6 09syk6 ciona savignyi

45 25 15.9 380 10 Q95QUL 095qul arabidopsis

RESULT 1

ID Q9D7Q2 PRELIMINARY PRT; 102 AA.

09D7Q2; DT 01-JUN-2001 (TREMBLrel. 17, Created)

DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE 2300002G24RIK protein.

GN Q9D7Q2

OS Mus musculus (Mouse)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.

NCBI\_TaxID=10090; [1]

RN RP SEQUENCE FROM N.A.

RP STRAIN=C57BL/6J; TISSUE-TONGUE;

RX MEDLINE=21085650; PUBMED=11217851;

RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamamoto T., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matudaka H.A., Ashburner M., Balatov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Koichi H., Schriml L.M., Lewis S., Matsuo Y., Niihido T., Peso G., Quackenbush J., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carrinci P., de Bonaldo M.F., Broomstein M.J., Bult C., Flercher C., Fujita M., Garibaldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima T., Mazzarelli J., Mombraerts P., Nordone P., Ring M., Rodriguez T., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyoda K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsuki S., Hayashizaki Y., "Functional annotation of a full-length mouse cDNA collection.", MGD; MGI; 1921425; 2300002G24RIK.



DT 01-MAY-1999 (TREMBLrel. 10, last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)  
 DE TRAM protein.  
 RN GN Shigella sonnei.  
 OG Plasmid Colib-P9.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Shigella.  
 OX NCBI\_TAXID=624;  
 RN [1]  
 SEQUENCE FROM N.A.  
 RC STRAIN=P9;  
 RA Sampei G., Mizobuchi K.;  
 RT "Organization and diversification of plasmid genomes: complete  
 nucleotide sequence of the Colib-P9 genome.";  
 RT Submitted (DNC-1998) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; AB021078; BAA75159.1; -.  
 KW Plasmid.  
 SQ SEQUENCE 230 AA; 25561 MW; FEE050BB13F09FA1 CRC64;  
 Query Match 16.6%; Score 26; DB 2; Length 230;  
 Best Local Similarity 30.8%; Pred. No. 7.8e+02;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
 QY 17 PXXXXXXCGXC 29  
 | | | | |  
 Db 38 PALIKALLCTGTC 50

RESULT 6

Q9R2H2 PRELIMINARY; PRT; 230 AA.

ID Q9R2H2  
 AC Q9R2H2;  
 DT 01-MAY-2000 (TREMBLrel. 13, created)  
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)  
 DE TRAM protein.  
 GN Salmonella typhimurium.  
 OS Plasmid R64.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Salmonella.  
 OX NCBI\_TaxID=602;  
 RN [1]  
 SEQUENCE FROM N.A.  
 RC STRAIN=DRD-11;  
 RA Komano T., Narahara K., Yoshida T., Furuya N.;  
 RT "The transfer region of IncII plasmid R64: similarities between R64  
 tra genes and *Legionella icm-dot* genes";  
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 SEQUENCE FROM N.A.  
 RC STRAIN=DRD-11;  
 RX MEDLINE-92011438; PubMed=1917882;  
 RA Furuya N., Komano T.;  
 RT "Determination of the nick site at oriT of IncII plasmid R64: global  
 similarity of oriT structures of IncII and IncP plasmids";  
 RL J. Bacteriol. 173:6612-6617(1991).  
 RN [3]  
 SEQUENCE FROM N.A.  
 RC STRAIN=DRD-11;  
 RX MEDLINE-9853641; PubMed=9393692;  
 RA Furuya N., Komano T.;  
 RT "Mutational analysis of the R64 oriT region: requirement for precise  
 location of the NtrA-binding sequence";  
 RL J. Bacteriol. 179:7291-7297(1997).  
 RN [4]  
 SEQUENCE FROM N.A.  
 RC STRAIN=DRD-11;  
 RX MEDLINE-9826896; PubMed=9603870;  
 RA Yoshida T., Furuya N., Ishikura M., Isobe T., Haino-Fukushima K.,  
 RA Ogawa T., Komano T.;  
 RN "Purification and characterization of thin pili of IncII plasmids

RESULT 7

Q9SDK7 PRELIMINARY; PRT; 240 AA.

ID Q9SDK7  
 AC Q9SDK7;  
 DT 01-MAY-2000 (TREMBLrel. 13, created)  
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)  
 DE Hypothetical protein.  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Oryzeae; Oryzae; Oryza.  
 OX NCBI\_TaxID=4530;  
 RN [1]  
 SEQUENCE FROM N.A.  
 RC STRAIN=CV\_NIPPONBARE;  
 RA Sasaki T., Matsumoto T., Yamamoto K.;  
 RT "Oryza sativa nippobare(GA3) genomic DNA, chromosome 1, PAC  
 clone:P0705D01";  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AP000492; BAA4609.1; -.  
 KW Hypothetical protein.  
 SQ SEQUENCE 240 AA; 2633 MW; E67BC59CB618FB3 CRC64;  
 Query Match 16.6%; Score 26; DB 10; Length 240;  
 Best Local Similarity 30.8%; Pred. No. 8e+02;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

RESULT 8

Q9HT3 PRELIMINARY; PRT; 257 AA.

ID Q9HT3  
 AC Q9HT3;  
 DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)

RN [5]  
 SEQUENCE FROM N.A.  
 RC STRAIN=DRD-11;  
 RA Pansegrau W., Schroder W., Lanka E.;  
 RT "Concerted action of three distinct domains in the DNA cleaving-joining reaction catalyzed by relaxase (Tral) of conjugative plasmid RP4";  
 RL J. Biol. Chem. 269:2782-2789(1994).  
 RN [6]  
 SEQUENCE FROM N.A.  
 RC STRAIN=DRD-11;  
 RA MEDLINE=94132048; PubMed=8300611;  
 RA Pansegrau W., Schroder W., Lanka E.;  
 RT "Concerted action of three distinct domains in the DNA cleaving-joining reaction catalyzed by relaxase (Tral) of conjugative plasmid RP4";  
 RL J. Biol. Chem. 269:2782-2789(1994).  
 RN [7]  
 SEQUENCE FROM N.A.  
 RC STRAIN=DRD-11;  
 RA MEDLINE=9485211; PubMed=8014987;  
 RA Pansegrau W., Lanka E., Barth P.T., Figurski D.H., Guiney D.G.,  
 RA Haas D., Helinski D.R., Schwab H., Stasiwski V.A., Thomas C.M.,  
 RA "Complete nucleotide sequence of Birmingham IncP-alpha plasmids: compilation and comparative analysis.>";  
 RT J. Mol. Biol. 239:623-663(1994).  
 RL EMBL; AB027308; BAA78001.1; -.  
 DR Plasmid.  
 KW SEQUENCE 230 AA; 25560 MW; F43394751D05AB90 CRC64;  
 Query Match 16.6%; Score 26; DB 2; Length 230;  
 Best Local Similarity 30.8%; Pred. No. 7.8e+02;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
 DE CDNA FLJ14280 fis, clone PLACE1005584, weakly similar to trans-acting  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OX NCBI\_TaxID=9606;  
 RN [1];  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=PLACENTA;  
 RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,  
 RA Nishikawa T., Nai K., Sugano S., Shiratori A., Sudo H.,  
 RA Nagatsuna M., Hosoi T., Kaku Y., Kodaira H., Sugawara M.,  
 RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,  
 RA Yamamoto S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,  
 RA Ninomiya K., Inayangi T.;  
 RA "NEDO human cDNA sequencing project";  
 RL Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AK024342; BAB14892.1; -.  
 SQ SEQUENCE 257 AA; 26269 MW; B914A57EA54D418 CRC64;  
 Query Match 16.6%; Score 26; DB 4; Length 257;  
 Best Local Similarity 30.8%; Pred. No. 8.3e+02; 0; Mismatches 0; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 17 PXXXXXXCGXC 29  
 Db 179 PLCSYRTSCAGSC 191

RESULT 9  
 017764 PRELIMINARY; PRT; 278 AA.  
 ID 017764  
 AC 017764;  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DE FO1G10.6 protein.  
 GN FO1G10.6  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nemata; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Palaeoderrinae; Caenorhabditis; [1]  
 RN NCBI\_TaxID=6339;  
 RP SEQUENCE FROM N.A.  
 RA Hembry C.;  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.  
 RN [2];  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99069613; PubMed=9851916;  
 RA none;  
 RT "Genome sequence of the nematode *C.elegans*: A platform for  
 investigating biology";  
 RL Science 282:2012-2018(1998);  
 DR EMBL; 281585; CAB0461.1; -.  
 SQ SEQUENCE 347 AA; 39762 MW; E97BA2961988A5A CRC64;  
 Query Match 16.6%; Score 26; DB 5; Length 347;  
 Best Local Similarity 30.8%; Pred. No. 9.6e+02; 0; Mismatches 9; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 17 PXXXXXXCGXC 29  
 Db 87 PLIATSGCFGIC 99

RESULT 11  
 Q8RZ09 PRELIMINARY; PRT; 349 AA.  
 ID Q8RZ09  
 AC Q8RZ09;  
 DT 01-JUN-2002 (TREMBLrel. 21, Created)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)  
 DE Hypothetical protein 39.1 kDa protein (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1];  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=COLON;  
 RA Strausberg R.;  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; BC022669; AAH22669.1; -.  
 KW Hypothetical protein.  
 FT NON\_TER  
 SQ SEQUENCE 349 AA; 39115 MW; D361C92578686F63 CRC64;  
 Query Match 16.6%; Score 26; DB 11; Length 349;  
 Best Local Similarity 30.8%; Pred. No. 9.7e+02; 0; Mismatches 9; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 17 PXXXXXXCGXC 29  
 Db 59 PSNTFABSCSGPC 71

RESULT 12  
 Q9DFC6 PRELIMINARY; PRT; 366 AA.  
 ID Q9DFC6  
 AC Q9DFC6;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 OS Xenopus laevis (African clawed frog).

RESULT 10  
 O18027 PRELIMINARY; PRT; 347 AA.  
 ID O18027  
 AC 018027;  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 Qy 17 PXXXXXXCGXC 29  
 Db 59 PSNTFABSCSGPC 71

	SQ	SEQUENCE	367 AA;	41504 MW;	DEA90275BC0574A CRC64;
OC		Eukaryota;	Metazoa;	Chordata;	Craniata;
OC					Vertebrata;
OC					Euteleostomi;
NCBI_TaxID=8355;					
[1]					
SEQUENCE FROM N.A.					
RX		Medline=20341055;	Pubmed=10882517;		
RA		Brantford W.W., Essner J.J., Yost H.J.;			
RT		"Regulation of gut and heart left-right asymmetry by context-dependent interactions between Xenopus lefty and BMP4 signaling.";			
RT		Dev. Biol. 223:291-306 (2000);			
RL		-1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.			
CC					
DR		EMBL; AF283562; AAG10034.1; -.			
DR		HSSP; P18075; 1BMP.			
DR		InterPro; IPR001839; TGFb.			
DR		InterPro; IPR001111; TGFb_N.			
PFAM		PF00019; TGF-beta; 1.			
DR		Pfam; PF00688; TGFb_propeptide; 1.			
DR		ProDom; PD000357; TGFb; 1.			
DR		SMART; SM00204; TGFb; 1.			
DR		PROSITE; PS00250; TGF_BETA_1; 1.			
KW		Glycoprotein.			
SQ		SEQUENCE 366 AA;	41434 MW;	E65C8C306F4B5ED5 CRC64;	
Query Match	QY	16.6%;	Score 26;	DB 13;	Length 367;
Best Local Similarity	QY	30.8%;	Pred. No. 9.9e-02;	DB 13;	Length 367;
Matches	QY	4;	Mismatches 0;	Indels 0;	Gaps 0;
Db	293	PAGYNAFRCTGSC 305			
RESULT 13					
Q9DD36	ID				
Q9DD36	PRELIMINARY;				
AC	PRT;	367 AA.			
Q9DD36;					
DT	01-MAR-2001 (TREMBLrel. 16, Created)				
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)				
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)				
XANTIVIN	(Lefty-related factor Xatv).				
OS	Xenopus laevis (African clawed frog).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;				
OC	Xenopodinae; Xenopus.				
RN					
SEQUENCE FROM N.A.					
RX		Pubmed=11091069;			
RA		Tanegashima K., Yokota C., Takahashi S., Asashima M.;			
RT		"Expression cloning of Xantivin, a Xenopus lefty/antivin-related gene, involved in the regulation of activin signaling during mesoderm induction.";			
RT		Mech. Dev. 99:3-14 (2000).			
RL					
RN					
SEQUENCE FROM N.A.					
RX		Cheng A.M.S., Thisse B., Thisse C., Wright C.V.E.;			
RT		"The Lefty-related factor Xatv acts as a feedback inhibitor of nodal signaling in mesoderm induction and L-R axis development in Xenopus.";			
RT		Development 0:0-0 (2000).			
RL		-1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.			
CC					
DR		EMBL; AB038010; BAB12725.1; -.			
DR		EMBL; AF209744; AG35771.1; -.			
DR		HSPP; P08112; 2TGFb.			
DR		InterPro; IPR001839; TGFb.			
DR		InterPro; IPR001111; TGFb_N.			
DR		PFAM; P00019; TGF-beta; 1.			
DR		InterPro; IPR001839; TGFb.			
DR		ProDom; PD000357; TGFb; 1.			
DR		SMART; SM00204; TGFb; 1.			
DR		PROSITE; PS00250; TGF_BETA_1; 1.			
KW		Glycoprotein.			
SQ		SEQUENCE 367 AA;	41604 MW;	DBA7E85752BF3A CRC64;	
Query Match	QY	16.6%;	Score 26;	DB 13;	Length 367;
Best Local Similarity	QY	30.8%;	Pred. No. 9.9e-02;	DB 13;	Length 367;
Matches	QY	4;	Mismatches 0;	Indels 0;	Gaps 0;
Db	293	PAGYNAFRCTGSC 305			
RESULT 15					
Q9P1Q2	ID				
Q9P1Q2	PRELIMINARY;				
AC	PRT;	376 AA.			
Q9P1Q2;					
DT	01-MAY-2000 (TREMBLrel. 13, Created)				
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)				
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)				
DE	Transforming growth factor beta precursor.				
OS	Common carp.				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butteleostomi;				
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;				
OC	Cyprinidae; Cyprinus.				
OX	NCBI_TaxID=792;				
RN					
RP		SEQUENCE FROM N.A.			
RA		Yin Z., Kuang J.;			
RT		"Molecular cloning of carp transforming growth factor beta 1.";			
RT		Submitter (MAR-1999) to the EMBL/GenBank/DBJ databases.			
CC		-1- FUNCTION: IS LIKELY TO BE AN IMPORTANT CYTOKINE REGULATING IMMUNE RESPONSE. MAY ALSO HAVE A ROLE IN OTHER PHYSIOLOGICAL SYSTEMS.			

CC -|- SUBUNIT; HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).  
 CC -|- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
 DR EMBL: AEL36947; AAC22573; 1; -.  
 DR HSSP: P01137; IKA.  
 DR InterPro: IPR001839; TGFb.  
 DR InterPro: IPR00111; TGFb\_N.  
 DR Pfam: PF00019; TGF-beta; 1.  
 DR Pfam: PF00688; TGFb; 1.  
 DR PRODOM: PD000357; TGFb; 1.  
 DR SMART: SM00204; TGF-BETA\_1.  
 DR PROSITE: PS00250; TGF-BETA\_1.  
 KW Growth factor; Mitogen; Glycoprotein; Signal.  
 KW SIGNAL 1  
 FT PROPEP 22  
 FT PROPEP 23  
 FT CHAIN 264  
 FT CHAIN 265  
 FT DISULFID 272  
 FT DISULFID 280  
 FT DISULFID 308  
 FT DISULFID 373  
 FT DISULFID 312  
 FT DISULFID 375  
 FT CARBOHD 341  
 FT CARBOHD 341  
 FT CARBOHD 76  
 FT CARBOHD 125  
 FT CARBOHD 125  
 FT SITE 167  
 FT SITE 230  
 SQ SEQUENCE 376 AA; 43329 MW; 7F7CC4DA58B69681 CRC64;  
 Query Match 16.6%; Score 26; DB 13; Length 376;  
 Best Local Similarity 30.8%; Pred. No. 1e+03; 0; Mismatches 0; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 17 PXXXXXXCXCXC 29  
 QY 17 PXXXXXXCXCXC 29  
 Db 300 PSGYVANYCTGSC 312

Search completed: March 27, 2003, 11:01:43  
 Job time : 87 secs